SEQUENCE LISTING

<110> The Government of the United States of America, as
represented by the Secretary, Department of Health and Human
Services, c/o Centers for Disease Control and Prevention
Chang, Gwong-Jen J.

<120> NUCLEIC ACID VACCINES FOR PREVENTION OF FLAVIVIRUS INFECTION

<130> 6395-64908

<150> PCT/US02/10764
<151> 2002-04-04

<150> 09/826,115
<151> 2001-04-04

<150> 09/701,536
<151> 2000-11-29

<150> PCT/US99/12298
<151> 1999-06-03

<150> 60/087,908
<151> 1998-06-04

<160> 61

<170> PatentIn version 3.2

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cgagcaaaat ttaagctaca acaaggcaag gcttgaccga caattgcatg aagaatctgc     180

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gattattgac tagttattaa tagtaatcaa ttacggggtc attagttcat agcccatata     300

tggagttccg cgttacataa cttacggtaa atggcccgcc tggctgaccg cccaacgacc     360

cccgcccatt gacgtcaata atgacgtatg ttcccatagt aacgccaata gggactttcc     420

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atgcccagta catgacctta tgggactttc ctacttggca gtacatctac gtattagtca     600

tcgctattac catggtgatg cggttttggc agtacatcaa tgggcgtgga tagcggtttg     660

actcacgggg atttccaagt ctccacccca ttgacgtcaa tgggagtttg ttttggcacc     720
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ctgcttactg gcttatcgaa attaatacga ctcactatag ggagacccaa gcttggtacc      900

gagctcgccg ccgcc atg ggc aga aag caa aac aaa aga gga gga aat gaa      951
             Met Gly Arg Lys Gln Asn Lys Arg Gly Gly Asn Glu
             1             5                   10

ggc tca atc atg tgg ctc gcg agc ttg gca gtt gtc ata gct tgt gcg      999
Gly Ser Ile Met Trp Leu Ala Ser Leu Ala Val Val Ile Ala Cys Ala
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gga gcc atg aag ttg tcg aat ttc cag ggg aag ctt ttg atg acc atc     1047
Gly Ala Met Lys Leu Ser Asn Phe Gln Gly Lys Leu Leu Met Thr Ile
    30                  35                  40

aac aac acg gac att gca gac gtt atc gtg att ccc acc tca aaa gga     1095
Asn Asn Thr Asp Ile Ala Asp Val Ile Val Ile Pro Thr Ser Lys Gly
45                  50                  55                  60

gag aac aga tgc tgg gtc cgg gca atc gac gtc ggc tac atg tgt gag     1143
Glu Asn Arg Cys Trp Val Arg Ala Ile Asp Val Gly Tyr Met Cys Glu
                65                  70                  75

gac act atc acg tac gaa tgt cct aag ctt acc atg ggc aat gat cca     1191
Asp Thr Ile Thr Tyr Glu Cys Pro Lys Leu Thr Met Gly Asn Asp Pro
                80                  85                  90

gag gat gtg gat tgc tgg tgt gac aac caa gaa gtc tac gtc caa tat     1239
Glu Asp Val Asp Cys Trp Cys Asp Asn Gln Glu Val Tyr Val Gln Tyr
            95                  100                 105

gga cgg tgc acg cgg acc agg cat tcc aag cga agc agg aga tcc gtg     1287
Gly Arg Cys Thr Arg Thr Arg His Ser Lys Arg Ser Arg Arg Ser Val
    110                 115                 120

tcg gtc caa aca cat ggg gag agt tca cta gtg aat aaa aaa gag gct     1335
Ser Val Gln Thr His Gly Glu Ser Ser Leu Val Asn Lys Lys Glu Ala
125                 130                 135                 140

tgg ctg gat tca acg aaa gcc aca cga tat ctc atg aaa act gag aac     1383
Trp Leu Asp Ser Thr Lys Ala Thr Arg Tyr Leu Met Lys Thr Glu Asn
                145                 150                 155

tgg atc ata agg aat cct ggc tat gct ttc ctg gcg gcg gta ctt ggc     1431
Trp Ile Ile Arg Asn Pro Gly Tyr Ala Phe Leu Ala Ala Val Leu Gly
                160                 165                 170

tgg atg ctt ggc agt aac aac ggt caa cgc gtg gta ttt acc atc ctc     1479
Trp Met Leu Gly Ser Asn Asn Gly Gln Arg Val Val Phe Thr Ile Leu
        175                 180                 185

ctg ctg ttg gtc gct ccg gct tac agt ttt aat tgt ctg gga atg ggc     1527
Leu Leu Leu Val Ala Pro Ala Tyr Ser Phe Asn Cys Leu Gly Met Gly
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aat cgt gac ttc ata gaa gga gcc agt gga gcc act tgg gtg gac ttg     1575
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Asn Arg Asp Phe Ile Glu Gly Ala Ser Gly Ala Thr Trp Val Asp Leu
205             210             215                     220

gtg ctg gaa gga gat agc tgc ttg aca atc atg gca aac gac aaa cca        1623
Val Leu Glu Gly Asp Ser Cys Leu Thr Ile Met Ala Asn Asp Lys Pro
                225             230             235

aca ttg gac gtc cgc atg att aac atc gaa gct agc caa ctt gct gag        1671
Thr Leu Asp Val Arg Met Ile Asn Ile Glu Ala Ser Gln Leu Ala Glu
            240             245             250

gtc aga agt tac tgc tat cat gct tca gtc act gac atc tcg acg gtg        1719
Val Arg Ser Tyr Cys Tyr His Ala Ser Val Thr Asp Ile Ser Thr Val
            255             260             265

gct cgg tgc ccc acg act gga gaa gcc cac aac gag aag cga gct gat        1767
Ala Arg Cys Pro Thr Thr Gly Glu Ala His Asn Glu Lys Arg Ala Asp
            270             275             280

agt agc tat gtg tgc aaa caa ggc ttc act gac cgt ggg tgg ggc aac        1815
Ser Ser Tyr Val Cys Lys Gln Gly Phe Thr Asp Arg Gly Trp Gly Asn
285             290             295                     300

gga tgt gga ctt ttc ggg aag gga agc att gac aca tgt gca aaa ttc        1863
Gly Cys Gly Leu Phe Gly Lys Gly Ser Ile Asp Thr Cys Ala Lys Phe
                305             310             315

tcc tgc acc agt aaa gcg att ggg aga aca atc cag cca gaa aac atc        1911
Ser Cys Thr Ser Lys Ala Ile Gly Arg Thr Ile Gln Pro Glu Asn Ile
                320             325             330

aaa tac gaa gtt ggc att ttt gtg cat gga acc acc act tcg gaa aac        1959
Lys Tyr Glu Val Gly Ile Phe Val His Gly Thr Thr Thr Ser Glu Asn
                335             340             345

cat ggg aat tat tca gcg caa gtt ggg gcg tcc cag gcg gca aag ttt        2007
His Gly Asn Tyr Ser Ala Gln Val Gly Ala Ser Gln Ala Ala Lys Phe
    350             355             360

aca gta aca ccc aat gct cct tcg ata acc ctc aaa ctt ggt gac tac        2055
Thr Val Thr Pro Asn Ala Pro Ser Ile Thr Leu Lys Leu Gly Asp Tyr
365             370             375                     380

gga gaa gtc aca ctg gac tgt gag cca agg agt gga ctg aac act gaa        2103
Gly Glu Val Thr Leu Asp Cys Glu Pro Arg Ser Gly Leu Asn Thr Glu
                385             390             395

gcg ttt tac gtc atg acc gtg ggg tca aag tca ttt ctg gtc cat agg        2151
Ala Phe Tyr Val Met Thr Val Gly Ser Lys Ser Phe Leu Val His Arg
                400             405             410

gag tgg ttt cat gac ctc gct ctc ccc tgg acg tcc cct tcg agc aca        2199
Glu Trp Phe His Asp Leu Ala Leu Pro Trp Thr Ser Pro Ser Ser Thr
                415             420             425

gcg tgg aga aac aga gaa ctc ctc atg gaa ttt gaa gag gcg cac gcc        2247
Ala Trp Arg Asn Arg Glu Leu Leu Met Glu Phe Glu Glu Ala His Ala
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aca aaa cag tcc gtt gtt gct ctt ggg tca cag gaa gga ggc ctc cat        2295
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Thr Lys Gln Ser Val Val Ala Leu Gly Ser Gln Glu Gly Gly Leu His
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cag gcg ttg gca gga gcc atc gtg gtg gag tac tca agc tca gtg aag      2343
Gln Ala Leu Ala Gly Ala Ile Val Val Glu Tyr Ser Ser Ser Val Lys
              465           470           475

tta aca tca ggc cac ctg aaa tgt agg ctg aaa atg gac aaa ctg gct      2391
Leu Thr Ser Gly His Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Ala
              480           485           490

ctg aaa ggc aca acc tat ggc atg tgt aca gaa aaa ttc tcg ttc gcg      2439
Leu Lys Gly Thr Thr Tyr Gly Met Cys Thr Glu Lys Phe Ser Phe Ala
              495           500           505

aaa aat ccg gcg gac act ggt cac gga aca gtt gtc att gaa ctc tcc      2487
Lys Asn Pro Ala Asp Thr Gly His Gly Thr Val Val Ile Glu Leu Ser
              510           515           520

tac tct ggg agt gat ggc ccc tgc aaa att ccg att gct tcc gtt gcg      2535
Tyr Ser Gly Ser Asp Gly Pro Cys Lys Ile Pro Ile Ala Ser Val Ala
525           530           535           540

agc ctc aat gac atg acc ccc gtt ggg cgg ctg gtg aca gtg aac ccc      2583
Ser Leu Asn Asp Met Thr Pro Val Gly Arg Leu Val Thr Val Asn Pro
              545           550           555

ttc gtc gcg act tcc agt gcc agc tca aag gtg ctg gtc gag atg gaa      2631
Phe Val Ala Thr Ser Ser Ala Ser Ser Lys Val Leu Val Glu Met Glu
              560           565           570

ccc ccc ttc gga gac tcc tac atc gta gtt gga agg gga gac aag cag      2679
Pro Pro Phe Gly Asp Ser Tyr Ile Val Val Gly Arg Gly Asp Lys Gln
              575           580           585

atc aac cac cat tgg cac aaa gct gga agc acg ctg ggc aag gcc ttt      2727
Ile Asn His His Trp His Lys Ala Gly Ser Thr Leu Gly Lys Ala Phe
              590           595           600

tca aca act ttg aag gga gct caa aga ctg gca gcg ttg ggc gac aca      2775
Ser Thr Thr Leu Lys Gly Ala Gln Arg Leu Ala Ala Leu Gly Asp Thr
605           610           615           620

gcc tgg gac ttt ggc tct att gga ggg gtc ttc aac tcc ata gga aaa      2823
Ala Trp Asp Phe Gly Ser Ile Gly Gly Val Phe Asn Ser Ile Gly Lys
              625           630           635

gcc gtt cac caa gtg ttt ggt ggt gcc ttc aga aca ctc ttt ggg gga      2871
Ala Val His Gln Val Phe Gly Gly Ala Phe Arg Thr Leu Phe Gly Gly
              640           645           650

atg tct tgg atc aca caa ggg cta atg ggt gcc cta ctg ctc tgg atg      2919
Met Ser Trp Ile Thr Gln Gly Leu Met Gly Ala Leu Leu Leu Trp Met
              655           660           665

ggc gtc aac gca cga gac cga tca att gct ttg gcc ttc tta gcc aca      2967
Gly Val Asn Ala Arg Asp Arg Ser Ile Ala Leu Ala Phe Leu Ala Thr
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7

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<220>
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Leu Ser Asn Phe Gln Gly Lys Leu Leu Met Thr Ile Asn Asn Thr Asp
        35                  40                  45


Ile Ala Asp Val Ile Val Ile Pro Thr Ser Lys Gly Glu Asn Arg Cys
    50                  55                  60
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10

Trp Val Arg Ala Ile Asp Val Gly Tyr Met Cys Glu Asp Thr Ile Thr
65   70   75   80

Tyr Glu Cys Pro Lys Leu Thr Met Gly Asn Asp Pro Glu Asp Val Asp
                85   90   95

Cys Trp Cys Asp Asn Gln Glu Val Tyr Val Gln Tyr Gly Arg Cys Thr
            100   105   110

Arg Thr Arg His Ser Lys Arg Ser Arg Arg Ser Val Ser Val Gln Thr
            115   120   125

His Gly Glu Ser Ser Leu Val Asn Lys Lys Glu Ala Trp Leu Asp Ser
    130   135   140

Thr Lys Ala Thr Arg Tyr Leu Met Lys Thr Glu Asn Trp Ile Ile Arg
145   150   155   160

Asn Pro Gly Tyr Ala Phe Leu Ala Ala Val Leu Gly Trp Met Leu Gly
            165   170   175

Ser Asn Asn Gly Gln Arg Val Val Phe Thr Ile Leu Leu Leu Leu Val
            180   185   190

Ala Pro Ala Tyr Ser Phe Asn Cys Leu Gly Met Gly Asn Arg Asp Phe
    195   200   205

Ile Glu Gly Ala Ser Gly Ala Thr Trp Val Asp Leu Val Leu Glu Gly
    210   215   220

Asp Ser Cys Leu Thr Ile Met Ala Asn Asp Lys Pro Thr Leu Asp Val
225   230   235   240

Arg Met Ile Asn Ile Glu Ala Ser Gln Leu Ala Glu Val Arg Ser Tyr
            245   250   255

Cys Tyr His Ala Ser Val Thr Asp Ile Ser Thr Val Ala Arg Cys Pro
            260   265   270

Thr Thr Gly Glu Ala His Asn Glu Lys Arg Ala Asp Ser Ser Tyr Val
            275   280   285

Cys Lys Gln Gly Phe Thr Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu
    290   295   300

11

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Phe Gly Lys Gly Ser Ile Asp Thr Cys Ala Lys Phe Ser Cys Thr Ser
305             310             315             320


Lys Ala Ile Gly Arg Thr Ile Gln Pro Glu Asn Ile Lys Tyr Glu Val
            325             330             335


Gly Ile Phe Val His Gly Thr Thr Thr Ser Glu Asn His Gly Asn Tyr
            340             345             350


Ser Ala Gln Val Gly Ala Ser Gln Ala Ala Lys Phe Thr Val Thr Pro
            355             360             365


Asn Ala Pro Ser Ile Thr Leu Lys Leu Gly Asp Tyr Gly Glu Val Thr
    370             375             380


Leu Asp Cys Glu Pro Arg Ser Gly Leu Asn Thr Glu Ala Phe Tyr Val
385             390             395             400


Met Thr Val Gly Ser Lys Ser Phe Leu Val His Arg Glu Trp Phe His
            405             410             415


Asp Leu Ala Leu Pro Trp Thr Ser Pro Ser Ser Thr Ala Trp Arg Asn
            420             425             430


Arg Glu Leu Leu Met Glu Phe Glu Glu Ala His Ala Thr Lys Gln Ser
            435             440             445


Val Val Ala Leu Gly Ser Gln Glu Gly Gly Leu His Gln Ala Leu Ala
    450             455             460


Gly Ala Ile Val Val Glu Tyr Ser Ser Ser Val Lys Leu Thr Ser Gly
465             470             475             480


His Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Ala Leu Lys Gly Thr
            485             490             495


Thr Tyr Gly Met Cys Thr Glu Lys Phe Ser Phe Ala Lys Asn Pro Ala
            500             505             510


Asp Thr Gly His Gly Thr Val Val Ile Glu Leu Ser Tyr Ser Gly Ser
            515             520             525


Asp Gly Pro Cys Lys Ile Pro Ile Ala Ser Val Ala Ser Leu Asn Asp
    530             535             540
```

12

```
Met Thr Pro Val Gly Arg Leu Val Thr Val Asn Pro Phe Val Ala Thr
545               550               555               560


Ser Ser Ala Ser Ser Lys Val Leu Val Glu Met Glu Pro Pro Phe Gly
                565               570               575


Asp Ser Tyr Ile Val Val Gly Arg Gly Asp Lys Gln Ile Asn His His
            580               585               590


Trp His Lys Ala Gly Ser Thr Leu Gly Lys Ala Phe Ser Thr Thr Leu
        595               600               605


Lys Gly Ala Gln Arg Leu Ala Ala Leu Gly Asp Thr Ala Trp Asp Phe
    610               615               620


Gly Ser Ile Gly Gly Val Phe Asn Ser Ile Gly Lys Ala Val His Gln
625               630               635               640


Val Phe Gly Gly Ala Phe Arg Thr Leu Phe Gly Gly Met Ser Trp Ile
            645               650               655


Thr Gln Gly Leu Met Gly Ala Leu Leu Leu Trp Met Gly Val Asn Ala
            660               665               670


Arg Asp Arg Ser Ile Ala Leu Ala Phe Leu Ala Thr Gly Gly Val Leu
        675               680               685


Val Phe Leu Ala Thr Asn Val His Ala
    690               695
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<210> 12
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
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<220>
<221> misc_feature
<222> (1)..(46)
<223> WN 466

<400> 12
cttggtaccc gtctcggcgc cgtgaccctc tcgaacttcc agggca   46

<210> 13
<211> 43

<212> DNA
<213> Artificial Sequence

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<220>
<221> misc_feature
<222> (1)..(43)
<223> CWN2444

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agaggcactt gcacgtgcgg acttccgccg gcgaaaaaga aaa   43

<210> 14
<211> 24
<212> PRT
<213> Artificial Sequence

<220>
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<220>
<221> MISC_FEATURE
<223> JE Signal

<400> 14

Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala Ser Leu Ala
1   5   10   15

Val Val Ile Ala Cys Ala Gly Ala
            20

<210> 15
<211> 5308
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note = synthetic construct

<220>
<221> misc_feature
<222> (1)..(5308)
<223> pCBWN

<220>
<221> CDS
<222> (911)..(2986)

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gacggatcgg gagatctccc gatcccctat ggtgcactct cagtacaatc tgctctgatg   60

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ccgcatagtt aagccagtat ctgctccctg cttgtgtgtt ggaggtcgct gagtagtgcg      120

cgagcaaaat ttaagctaca acaaggcaag gcttgaccga caattgcatg aagaatctgc      180

ttagggttag gcgttttgcg ctgcttcgcg atgtacgggc cagatatacg cgttgacatt      240·

gattattgac tagttattaa tagtaatcaa ttacggggtc attagttcat agcccatata      300

tggagttccg cgttacataa cttacggtaa atggcccgcc tggctgaccg cccaacgacc      360

cccgcccatt gacgtcaata atgacgtatg ttcccatagt aacgccaata gggactttcc      420

attgacgtca atgggtggag tatttacggt aaactgccca cttggcagta catcaagtgt      480

atcatatgcc aagtacgccc cctattgacg tcaatgacgg taaatggccc gcctggcatt      540

atgcccagta catgacctta tgggactttc ctacttggca gtacatctac gtattagtca      600

tcgctattac catggtgatg cggttttttgg cagtacatca atgggcgtgg atagcggttt      660

gactcacggg gatttccaag tctccacccc attgacgtca atgggagttt gttttggcac      720

caaaatcaac gggactttcc aaaatgtcgt aacaactccg ccccattgac gcaaatgggc      780

ggtaggcgtg tacggtggga ggtctatata agcagagctc tctggctaac tagagaaccc      840

actgcttact ggcttatcga aattaatacg actcactata gggagaccca agcttggtac      900

cgccgccgcc atg ggc aag agg tcc gcc ggc tca atc atg tgg ctc gcg       949
            Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala
             1           5                   10

agc ttg gca gtt gtc ata gct tgt gca ggc gcc gtg acc ctc tcg aac       997
Ser Leu Ala Val Val Ile Ala Cys Ala Gly Ala Val Thr Leu Ser Asn
     15              20                  25

ttc cag ggc aag gtg atg atg acg gta aat gct act gac gtc aca gat      1045
Phe Gln Gly Lys Val Met Met Thr Val Asn Ala Thr Asp Val Thr Asp
30              35                  40                  45

gtc atc acg att cca aca gct gct gga aag aac cta tgc att gtc aga      1093
Val Ile Thr Ile Pro Thr Ala Ala Gly Lys Asn Leu Cys Ile Val Arg
                 50                  55                  60

gca atg gat gtg gga tac atg tgc gat gat act atc act tat gaa tgc      1141
Ala Met Asp Val Gly Tyr Met Cys Asp Asp Thr Ile Thr Tyr Glu Cys
                 65                  70                  75

cca gtg ctg tcg gct ggt aat gat cca gaa gac atc gac tgt tgg tgc      1189
Pro Val Leu Ser Ala Gly Asn Asp Pro Glu Asp Ile Asp Cys Trp Cys
             80                  85                  90

aca aag tca gca gtc tac gtc agg tat gga aga tgc acc aag aca cgc      1237
Thr Lys Ser Ala Val Tyr Val Arg Tyr Gly Arg Cys Thr Lys Thr Arg
     95                  100                 105

cac tca aga cgc agt cgg agg tca ctg aca gtg cag aca cac gga gaa      1285
His Ser Arg Arg Ser Arg Arg Ser Leu Thr Val Gln Thr His Gly Glu
110                 115                 120                 125
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15

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agc act cta gcg aac aag aag ggg gct tgg atg gac agc acc aag gcc       1333
Ser Thr Leu Ala Asn Lys Lys Gly Ala Trp Met Asp Ser Thr Lys Ala
            130                 135                 140

aca agg tat ttg gta aaa aca gaa tca tgg atc ttg agg aac cct gga       1381
Thr Arg Tyr Leu Val Lys Thr Glu Ser Trp Ile Leu Arg Asn Pro Gly
            145                 150                 155

tat gcc ctg gtg gca gcc gtc att ggt tgg atg ctt ggg agc aac acc       1429
Tyr Ala Leu Val Ala Ala Val Ile Gly Trp Met Leu Gly Ser Asn Thr
            160                 165                 170

atg cag aga gtt gtg ttt gtc gtg cta ttg ctt ttg gtg gcc cca gct       1477
Met Gln Arg Val Val Phe Val Val Leu Leu Leu Leu Val Ala Pro Ala
            175                 180                 185

tac agc ttc aac tgc ctt gga atg agc aac aga gac ttc ttg gaa gga       1525
Tyr Ser Phe Asn Cys Leu Gly Met Ser Asn Arg Asp Phe Leu Glu Gly
190                 195                 200                 205

gtg tct gga gca aca tgg gtg gat ttg gtt ctc gaa ggc gac agc tgc       1573
Val Ser Gly Ala Thr Trp Val Asp Leu Val Leu Glu Gly Asp Ser Cys
            210                 215                 220

gtg act atc atg tct aag gac aag cct acc atc gat gtg aag atg atg       1621
Val Thr Ile Met Ser Lys Asp Lys Pro Thr Ile Asp Val Lys Met Met
            225                 230                 235

aat atg gag gcg gcc aac ctg gca gag gtc cgc agt tat tgc tat ttg       1669
Asn Met Glu Ala Ala Asn Leu Ala Glu Val Arg Ser Tyr Cys Tyr Leu
            240                 245                 250

gct acc gtc agc gat ctc tcc acc aaa gct gcg tgc ccg acc atg gga       1717
Ala Thr Val Ser Asp Leu Ser Thr Lys Ala Ala Cys Pro Thr Met Gly
            255                 260                 265

gaa gct cac aat gac aaa cgt gct gac cca gct ttt gtg tgc aga caa       1765
Glu Ala His Asn Asp Lys Arg Ala Asp Pro Ala Phe Val Cys Arg Gln
270                 275                 280                 285

gga gtg gtg gac agg ggc tgg ggc aac ggc tgc gga cta ttt ggc aaa       1813
Gly Val Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys
            290                 295                 300

gga agc att gac aca tgc gcc aaa ttt gcc tgc tct acc aag gca ata       1861
Gly Ser Ile Asp Thr Cys Ala Lys Phe Ala Cys Ser Thr Lys Ala Ile
            305                 310                 315

gga aga acc atc ttg aaa gag aat atc aag tac gaa gtg gcc att ttt       1909
Gly Arg Thr Ile Leu Lys Glu Asn Ile Lys Tyr Glu Val Ala Ile Phe
            320                 325                 330

gtc cat gga cca act act gtg gag tcg cac gga aac tac tcc aca cag       1957
Val His Gly Pro Thr Thr Val Glu Ser His Gly Asn Tyr Ser Thr Gln
            335                 340                 345

gtt gga gcc act cag gca ggg aga ttc agc atc act cct gcg gcg cct       2005
Val Gly Ala Thr Gln Ala Gly Arg Phe Ser Ile Thr Pro Ala Ala Pro
350                 355                 360                 365
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16

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tca tac aca cta aag ctt gga gaa tat gga gag gtg aca gtg gac tgt    2053
Ser Tyr Thr Leu Lys Leu Gly Glu Tyr Gly Glu Val Thr Val Asp Cys
            370                 375                 380

gaa cca cgg tca ggg att gac acc aat gca tac tac gtg atg act gtt    2101
Glu Pro Arg Ser Gly Ile Asp Thr Asn Ala Tyr Tyr Val Met Thr Val
            385                 390                 395

gga aca aag acg ttc ttg gtc cat cgt gag tgg ttc atg gac ctc aac    2149
Gly Thr Lys Thr Phe Leu Val His Arg Glu Trp Phe Met Asp Leu Asn
            400                 405                 410

ctc cct tgg agc agt gct gga agt act gtg tgg agg aac aga gag acg    2197
Leu Pro Trp Ser Ser Ala Gly Ser Thr Val Trp Arg Asn Arg Glu Thr
            415                 420                 425

tta atg gag ttt gag gaa cca cac gcc acg aag cag tct gtg ata gca    2245
Leu Met Glu Phe Glu Glu Pro His Ala Thr Lys Gln Ser Val Ile Ala
430                 435                 440                 445

ttg ggc tca caa gag gga gct ctg cat caa gct ttg gct gga gcc att    2293
Leu Gly Ser Gln Glu Gly Ala Leu His Gln Ala Leu Ala Gly Ala Ile
            450                 455                 460

cct gtg gaa ttt tca agc aac act gtc aag ttg acg tcg ggt cat ttg    2341
Pro Val Glu Phe Ser Ser Asn Thr Val Lys Leu Thr Ser Gly His Leu
            465                 470                 475

aag tgt aga gtg aag atg gaa aaa ttg cag ttg aag gga aca acc tat    2389
Lys Cys Arg Val Lys Met Glu Lys Leu Gln Leu Lys Gly Thr Thr Tyr
            480                 485                 490

ggc gtc tgt tca aag gct ttc aag ttt ctt ggg act ccc gcg gac aca    2437
Gly Val Cys Ser Lys Ala Phe Lys Phe Leu Gly Thr Pro Ala Asp Thr
            495                 500                 505

ggt cac ggc act gtg gtg ttg gaa ttg cag tac act ggc acg gat gga    2485
Gly His Gly Thr Val Val Leu Glu Leu Gln Tyr Thr Gly Thr Asp Gly
510                 515                 520                 525

cct tgc aaa gtt cct atc tcg tca gtg gct tca ttg aac gac cta acg    2533
Pro Cys Lys Val Pro Ile Ser Ser Val Ala Ser Leu Asn Asp Leu Thr
            530                 535                 540

cca gtg ggc aga ttg gtc act gtc aac cct ttt gtt tca gtg gcc acg    2581
Pro Val Gly Arg Leu Val Thr Val Asn Pro Phe Val Ser Val Ala Thr
            545                 550                 555

gcc aac gct aag gtc ctg att gaa ttg gaa cca ccc ttt gga gac tca    2629
Ala Asn Ala Lys Val Leu Ile Glu Leu Glu Pro Pro Phe Gly Asp Ser
            560                 565                 570

tac ata gtg gtg ggc aga gga gaa caa cag atc aat cac cat tgg cac    2677
Tyr Ile Val Val Gly Arg Gly Glu Gln Gln Ile Asn His His Trp His
            575                 580                 585

aag tct gga agc agc att ggc aaa gcc ttt aca acc acc ctc aaa gga    2725
Lys Ser Gly Ser Ser Ile Gly Lys Ala Phe Thr Thr Thr Leu Lys Gly
590                 595                 600                 605
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17

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gcg cag aga cta gcc gct cta gga gac aca gct tgg gac ttt gga tca        2773
Ala Gln Arg Leu Ala Ala Leu Gly Asp Thr Ala Trp Asp Phe Gly Ser
            610                 615                 620

gtt gga ggg gtg ttc acc tca gtt ggg aag gct gtc cat caa gtg ttc        2821
Val Gly Gly Val Phe Thr Ser Val Gly Lys Ala Val His Gln Val Phe
            625                 630                 635

gga gga gca ttc cgc tca ctg ttc gga ggc atg tcc tgg ata acg caa        2869
Gly Gly Ala Phe Arg Ser Leu Phe Gly Gly Met Ser Trp Ile Thr Gln
            640                 645                 650

gga ttg ctg ggg gct ctc ctg ttg tgg atg ggc atc aat gct cgt gat        2917
Gly Leu Leu Gly Ala Leu Leu Leu Trp Met Gly Ile Asn Ala Arg Asp
        655                 660                 665

agg tcc ata gct ctc acg ttt ctc gca gtt gga gga gtt ctg ctc ttc        2965
Arg Ser Ile Ala Leu Thr Phe Leu Ala Val Gly Gly Val Leu Leu Phe
670                 675                 680                 685

ctc tcc gtg aac gtg cac gcc tgaaggcggc cgctcgagca tgcatctaga         3016
Leu Ser Val Asn Val His Ala
                690

gggccctatt ctatagtgtc acctaaatgc tagagctcgc tgatcagcct cgactgtgcc    3076

ttctagttgc cagccatctg ttgtttgccc ctcccccgtg ccttccttga ccctggaagg    3136

tgccactccc actgtccttt cctaataaaa tgaggaaatt gcatcgcatt gtctgagtag    3196

gtgtcattct attctggggg gtggggtggg gcaggacagc aagggggagg attgggaaga    3256

caatagcagg catgctgggg atgcggtggg ctctatggct tctgaggcgg aaagaaccag    3316

ctgcattaat gaatcggcca acgcgcgggg agaggcggtt tgcgtattgg gcgctcttcc    3376

gcttcctcgc tcactgactc gctgcgctcg tcgttcggc tgcggcgagc ggtatcagct     3436

cactcaaagg cggtaatacg gttatccaca gaatcagggg ataacgcagg aaagaacatg    3496

tgagcaaaag gccagcaaaa ggccaggaac cgtaaaaagg ccgcgttgct ggcgtttttc    3556

cataggctcc gcccccctga cgagcatcac aaaaatcgac gctcaagtca gaggtggcga    3616

aacccgacag gactataaag ataccaggcg tttccccctg gaagctccct cgtgcgctct    3676

cctgttccga ccctgccgct taccggatac ctgtccgcct ttctcccttc gggaagcgtg    3736

gcgctttctc atagctcacg ctgtaggtat ctcagttcgg tgtaggtcgt tcgctccaag    3796

ctgggctgtg tgcacgaacc ccccgttcag cccgaccgct gcgccttatc cggtaactat    3856

cgtcttgagt ccaacccggt aagacacgac ttatcgccac tggcagcagc cactggtaac    3916

aggattagca gagcgaggta tgtaggcggt gctacagagt tcttgaagtg gtggcctaac    3976

tacggctaca ctagaagaac agtatttggt atctgcgctc tgctgaagcc agttaccttc    4036

ggaaaaagag ttggtagctc ttgatccggc aaacaaacca ccgctggtag cggtggtttt    4096
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18

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tttgtttgca agcagcagat tacgcgcaga aaaaaggat ctcaagaaga tcctttgatc   4156

ttttctacgg ggtctgacgc tcagtggaac gaaaactcac gttaagggat tttggtcatg   4216

agattatcaa aaaggatctt cacctagatc cttttaaatt aaaaatgaag ttttaaatca   4276

atctaaagta tatatgagta aacttggtct gacagttacc aatgcttaat cagtgaggca   4336

cctatctcag cgatctgtct atttcgttca tccatagttg cctgactccc cgtcgtgtag   4396

ataactacga tacgggaggg cttaccatct ggccccagtg ctgcaatgat accgcgagac   4456

ccacgctcac cggctccaga tttatcagca ataaaccagc cagccggaag ggccgagcgc   4516

agaagtggtc ctgcaacttt atccgcctcc atccagtcta ttaattgttg ccgggaagct   4576

agagtaagta gttcgccagt taatagtttg cgcaacgttg ttgccattgc tacaggcatc   4636

gtggtgtcac gctcgtcgtt tggtatggct tcattcagct ccggttccca acgatcaagg   4696

cgagttacat gatcccccat gttgtgcaaa aaagcggtta gctccttcgg tcctccgatc   4756

gttgtcagaa gtaagttggc cgcagtgtta tcactcatgg ttatggcagc actgcataat   4816

tctcttactg tcatgccatc cgtaagatgc ttttctgtga ctggtgagta ctcaaccaag   4876

tcattctgag aatagtgtat gcggcgaccg agttgctctt gcccggcgtc aatacgggat   4936

aataccgcgc cacatagcag aactttaaaa gtgctcatca ttggaaaacg ttcttcgggg   4996

cgaaaactct caaggatctt accgctgttg agatccagtt cgatgtaacc cactcgtgca   5056

cccaactgat cttcagcatc ttttactttc accagcgttt ctgggtgagc aaaaacagga   5116

aggcaaaatg ccgcaaaaaa gggaataagg gcgacacgga atgttgaat actcatactc   5176

ttcctttttc aatattattg aagcatttat cagggttatt gtctcatgag cggatacata   5236

tttgaatgta tttagaaaaa taaacaaata ggggttccgc gcacatttcc ccgaaaagtg   5296

ccacctgacg tc                                                      5308


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<211>  692
<212>  PRT
<213>  Artificial Sequence

<220>
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<400>  16

Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala Ser Leu Ala
1               5                   10                  15


Val Val Ile Ala Cys Ala Gly Ala Val Thr Leu Ser Asn Phe Gln Gly
                20                  25                  30
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19

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Lys Val Met Met Thr Val Asn Ala Thr Asp Val Thr Asp Val Ile Thr
    35                  40                  45

Ile Pro Thr Ala Ala Gly Lys Asn Leu Cys Ile Val Arg Ala Met Asp
    50                  55                  60

Val Gly Tyr Met Cys Asp Asp Thr Ile Thr Tyr Glu Cys Pro Val Leu
65                  70                  75                  80

Ser Ala Gly Asn Asp Pro Glu Asp Ile Asp Cys Trp Cys Thr Lys Ser
                85                  90                  95

Ala Val Tyr Val Arg Tyr Gly Arg Cys Thr Lys Thr Arg His Ser Arg
            100                 105                 110

Arg Ser Arg Arg Ser Leu Thr Val Gln Thr His Gly Glu Ser Thr Leu
            115                 120                 125

Ala Asn Lys Lys Gly Ala Trp Met Asp Ser Thr Lys Ala Thr Arg Tyr
    130                 135                 140

Leu Val Lys Thr Glu Ser Trp Ile Leu Arg Asn Pro Gly Tyr Ala Leu
145                 150                 155                 160

Val Ala Ala Val Ile Gly Trp Met Leu Gly Ser Asn Thr Met Gln Arg
            165                 170                 175

Val Val Phe Val Val Leu Leu Leu Leu Val Ala Pro Ala Tyr Ser Phe
            180                 185                 190

Asn Cys Leu Gly Met Ser Asn Arg Asp Phe Leu Glu Gly Val Ser Gly
    195                 200                 205

Ala Thr Trp Val Asp Leu Val Leu Glu Gly Asp Ser Cys Val Thr Ile
    210                 215                 220

Met Ser Lys Asp Lys Pro Thr Ile Asp Val Lys Met Met Asn Met Glu
225                 230                 235                 240

Ala Ala Asn Leu Ala Glu Val Arg Ser Tyr Cys Tyr Leu Ala Thr Val
            245                 250                 255

Ser Asp Leu Ser Thr Lys Ala Ala Cys Pro Thr Met Gly Glu Ala His
            260                 265                 270
```

20

Asn Asp Lys Arg Ala Asp Pro Ala Phe Val Cys Arg Gln Gly Val Val
        275   280   285

Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser Ile
        290   295   300

Asp Thr Cys Ala Lys Phe Ala Cys Ser Thr Lys Ala Ile Gly Arg Thr
305   310   315   320

Ile Leu Lys Glu Asn Ile Lys Tyr Glu Val Ala Ile Phe Val His Gly
            325   330   335

Pro Thr Thr Val Glu Ser His Gly Asn Tyr Ser Thr Gln Val Gly Ala
        340   345   350

Thr Gln Ala Gly Arg Phe Ser Ile Thr Pro Ala Ala Pro Ser Tyr Thr
        355   360   365

Leu Lys Leu Gly Glu Tyr Gly Glu Val Thr Val Asp Cys Glu Pro Arg
    370   375   380

Ser Gly Ile Asp Thr Asn Ala Tyr Tyr Val Met Thr Val Gly Thr Lys
385   390   395   400

Thr Phe Leu Val His Arg Glu Trp Phe Met Asp Leu Asn Leu Pro Trp
            405   410   415

Ser Ser Ala Gly Ser Thr Val Trp Arg Asn Arg Glu Thr Leu Met Glu
        420   425   430

Phe Glu Glu Pro His Ala Thr Lys Gln Ser Val Ile Ala Leu Gly Ser
        435   440   445

Gln Glu Gly Ala Leu His Gln Ala Leu Ala Gly Ala Ile Pro Val Glu
    450   455   460

Phe Ser Ser Asn Thr Val Lys Leu Thr Ser Gly His Leu Lys Cys Arg
465   470   475   480

Val Lys Met Glu Lys Leu Gln Leu Lys Gly Thr Thr Tyr Gly Val Cys
            485   490   495

Ser Lys Ala Phe Lys Phe Leu Gly Thr Pro Ala Asp Thr Gly His Gly
            500   505   510

21

Thr Val Val Leu Glu Leu Gln Tyr Thr Gly Thr Asp Gly Pro Cys Lys
        515   520   525

Val Pro Ile Ser Ser Val Ala Ser Leu Asn Asp Leu Thr Pro Val Gly
        530   535   540

Arg Leu Val Thr Val Asn Pro Phe Val Ser Val Ala Thr Ala Asn Ala
545   550   555   560

Lys Val Leu Ile Glu Leu Glu Pro Pro Phe Gly Asp Ser Tyr Ile Val
                565   570   575

Val Gly Arg Gly Glu Gln Gln Ile Asn His His Trp His Lys Ser Gly
        580   585   590

Ser Ser Ile Gly Lys Ala Phe Thr Thr Thr Leu Lys Gly Ala Gln Arg
        595   600   605

Leu Ala Ala Leu Gly Asp Thr Ala Trp Asp Phe Gly Ser Val Gly Gly
        610   615   620

Val Phe Thr Ser Val Gly Lys Ala Val His Gln Val Phe Gly Gly Ala
625   630   635   640

Phe Arg Ser Leu Phe Gly Gly Met Ser Trp Ile Thr Gln Gly Leu Leu
                645   650   655

Gly Ala Leu Leu Leu Trp Met Gly Ile Asn Ala Arg Asp Arg Ser Ile
                660   665   670

Ala Leu Thr Phe Leu Ala Val Gly Gly Val Leu Leu Phe Leu Ser Val
        675   680   685

Asn Val His Ala
    690

<210>   17
<211>   5334
<212>   DNA
<213>   Artificial Sequence

<220>
<223>   Description of artificial sequence; note = synthetic construct

<220>
<221>   misc_feature

22

<222> (1)..(5334)
<223> pCBJE 1-14

<220>
<221> CDS
<222> (916)..(3006)

<400> 17
gacggatcgg gagatctccc gatcccctat ggtgcactct cagtacaatc tgctctgatg   60

ccgcatagtt aagccagtat ctgctccctg cttgtgtgtt ggaggtcgct gagtagtgcg   120

cgagcaaaat ttaagctaca acaaggcaag gcttgaccga caattgcatg aagaatctgc   180

ttagggttag gcgttttgcg ctgcttcgcg atgtacgggc cagatatacg cgttgacatt   240

gattattgac tagttattaa tagtaatcaa ttacggggtc attagttcat agcccatata   300

tggagttccg cgttacataa cttacggtaa atggcccgcc tggctgaccg cccaacgacc   360

cccgcccatt gacgtcaata atgacgtatg ttcccatagt aacgccaata gggactttcc   420

attgacgtca atgggtggag tatttacggt aaactgccca cttggcagta catcaagtgt   480

atcatatgcc aagtacgccc cctattgacg tcaatgacgg taaatggccc gcctggcatt   540

atgcccagta catgacctta tgggactttc ctacttggca gtacatctac gtattagtca   600

tcgctattac catggtgatg cggttttggc agtacatcaa tgggcgtgga tagcggtttg   660

actcacgggg atttccaagt ctccacccca ttgacgtcaa tgggagtttg ttttggcacc   720

aaaatcaacg ggactttcca aaatgtcgta caactccgc cccattgacg caaatgggcg   780

gtaggcgtgt acggtgggag gtctatataa gcagagctct ctggctaact agagaaccca   840

ctgcttactg gcttatcgaa attaatacga ctcactatag ggagacccaa gcttggtacc   900

tctagagccg ccgcc atg ggc aga aag caa aac aaa aga gga gga aat gaa   951
               Met Gly Arg Lys Gln Asn Lys Arg Gly Gly Asn Glu
                1   5   10

ggc tca atc atg tgg ctc gcg agc ttg gca gtt gtc ata gct tgt gcg   999
Gly Ser Ile Met Trp Leu Ala Ser Leu Ala Val Val Ile Ala Cys Ala
         15   20   25

gga gcc atg aag ttg tcg aat ttc cag ggg aag ctt ttg atg acc atc   1047
Gly Ala Met Lys Leu Ser Asn Phe Gln Gly Lys Leu Leu Met Thr Ile
     30   35   40

aac aac acg gac att gca gac gtt atc gtg att ccc acc tca aaa gga   1095
Asn Asn Thr Asp Ile Ala Asp Val Ile Val Ile Pro Thr Ser Lys Gly
45   50   55   60

gag aac aga tgc tgg gtc cgg gca atc gac gtc ggc tac atg tgt gag   1143
Glu Asn Arg Cys Trp Val Arg Ala Ile Asp Val Gly Tyr Met Cys Glu
                 65   70   75

gac act atc acg tac gaa tgt cct aag ctt acc atg ggc aat gat cca   1191
Asp Thr Ile Thr Tyr Glu Cys Pro Lys Leu Thr Met Gly Asn Asp Pro

23

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gag gat gtg gat tgc tgg tgt gac aac caa gaa gtc tac gtc caa tat        1239
Glu Asp Val Asp Cys Trp Cys Asp Asn Gln Glu Val Tyr Val Gln Tyr
        95                  100                 105

gga cgg tgc acg cgg acc agg cat tcc aag cga agc agg aga tcc gtg        1287
Gly Arg Cys Thr Arg Thr Arg His Ser Lys Arg Ser Arg Arg Ser Val
        110                 115                 120

tcg gtc caa aca cat ggg gag agt tca cta gtg aat aaa aaa gag gct        1335
Ser Val Gln Thr His Gly Glu Ser Ser Leu Val Asn Lys Lys Glu Ala
125                 130                 135                 140

tgg ctg gat tca acg aaa gcc aca cga tat ctc atg aaa act gag aac        1383
Trp Leu Asp Ser Thr Lys Ala Thr Arg Tyr Leu Met Lys Thr Glu Asn
                145                 150                 155

tgg atc ata agg aat cct ggc tat gct ttc ctg gcg gcg gta ctt ggc        1431
Trp Ile Ile Arg Asn Pro Gly Tyr Ala Phe Leu Ala Ala Val Leu Gly
                160                 165                 170

tgg atg ctt ggc agt aac aac ggt caa cgc gtg gta ttt acc atc ctc        1479
Trp Met Leu Gly Ser Asn Asn Gly Gln Arg Val Val Phe Thr Ile Leu
            175                 180                 185

ctg ctg ttg gtc gct ccg gct tac agt ttt aat tgt ctg gga atg ggc        1527
Leu Leu Leu Val Ala Pro Ala Tyr Ser Phe Asn Cys Leu Gly Met Gly
        190                 195                 200

aat cgt gac ttc ata gaa gga gcc agt gga gcc act tgg gtg gac ttg        1575
Asn Arg Asp Phe Ile Glu Gly Ala Ser Gly Ala Thr Trp Val Asp Leu
205                 210                 215                 220

gtg ctg gaa gga gat agc tgc ttg aca atc atg gca aac gac aaa cca        1623
Val Leu Glu Gly Asp Ser Cys Leu Thr Ile Met Ala Asn Asp Lys Pro
                225                 230                 235

aca ttg gac gtc cgc atg att aac atc gaa gct agc caa ctt gct gag        1671
Thr Leu Asp Val Arg Met Ile Asn Ile Glu Ala Ser Gln Leu Ala Glu
                240                 245                 250

gtc aga agt tac tgc tat cat gct tca gtc act gac atc tcg acg gtg        1719
Val Arg Ser Tyr Cys Tyr His Ala Ser Val Thr Asp Ile Ser Thr Val
                255                 260                 265

gct cgg tgc ccc acg act gga gaa gcc cac aac gag aag cga gct gat        1767
Ala Arg Cys Pro Thr Thr Gly Glu Ala His Asn Glu Lys Arg Ala Asp
        270                 275                 280

agt agc tat gtg tgc aaa caa ggc ttc act gac cgt ggg tgg ggc aac        1815
Ser Ser Tyr Val Cys Lys Gln Gly Phe Thr Asp Arg Gly Trp Gly Asn
285                 290                 295                 300

gga tgt gga ctt ttc ggg aag gga agc att gac aca tgt gca aaa ttc        1863
Gly Cys Gly Leu Phe Gly Lys Gly Ser Ile Asp Thr Cys Ala Lys Phe
                305                 310                 315

tcc tgc acc agt aaa gcg att ggg aga aca atc cag cca gaa aac atc        1911
Ser Cys Thr Ser Lys Ala Ile Gly Arg Thr Ile Gln Pro Glu Asn Ile
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24

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aaa tac gaa gtt ggc att ttt gtg cat gga acc acc act tcg gaa aac      1959·
Lys Tyr Glu Val Gly Ile Phe Val His Gly Thr Thr Thr Ser Glu Asn
        335                 340                 345

cat ggg aat tat tca gcg caa gtt ggg gcg tcc cag gcg gca aag ttt      2007
His Gly Asn Tyr Ser Ala Gln Val Gly Ala Ser Gln Ala Ala Lys Phe
        350                 355                 360

aca gta aca ccc aat gct cct tcg ata acc ctc aaa ctt ggt gac tac      2055
Thr Val Thr Pro Asn Ala Pro Ser Ile Thr Leu Lys Leu Gly Asp Tyr
365                 370                 375                 380

gga gaa gtc aca ctg gac tgt gag cca agg agt gga ctg aac act gaa      2103
Gly Glu Val Thr Leu Asp Cys Glu Pro Arg Ser Gly Leu Asn Thr Glu
                385                 390                 395

gcg ttt tac gtc atg acc gtg ggg tca aag tca ttt ctg gtc cat agg      2151
Ala Phe Tyr Val Met Thr Val Gly Ser Lys Ser Phe Leu Val His Arg
            400                 405                 410

gag tgg ttt cat gac ctc gct ctc ccc tgg acg tcc cct tcg agc aca      2199
Glu Trp Phe His Asp Leu Ala Leu Pro Trp Thr Ser Pro Ser Ser Thr
        415                 420                 425

gcg tgg aga aac aga gaa ctc ctc atg gaa ttt gaa gag gcg cac gcc      2247
Ala Trp Arg Asn Arg Glu Leu Leu Met Glu Phe Glu Glu Ala His Ala
        430                 435                 440

aca aaa cag tcc gtt gtt gct ctt ggg tca cag gaa gga ggc ctc cat      2295
Thr Lys Gln Ser Val Val Ala Leu Gly Ser Gln Glu Gly Gly Leu His
445                 450                 455                 460

cag gcg ttg gca gga gcc atc gtg gtg gag tac tca agc tca gtg aag      2343
Gln Ala Leu Ala Gly Ala Ile Val Val Glu Tyr Ser Ser Ser Val Lys
            465                 470                 475

tta aca tca ggc cac ctg aaa tgt agg ctg aaa atg gac aaa ctg gct      2391
Leu Thr Ser Gly His Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Ala
            480                 485                 490

ctg aaa ggc aca acc tat ggc atg tgt aca gaa aaa ttc tcg ttc gcg      2439
Leu Lys Gly Thr Thr Tyr Gly Met Cys Thr Glu Lys Phe Ser Phe Ala
            495                 500                 505

aaa aat ccg gcg gac act ggt cac gga aca gtt gtc att gaa ctc tcc      2487
Lys Asn Pro Ala Asp Thr Gly His Gly Thr Val Val Ile Glu Leu Ser
        510                 515                 520

tac tct ggg agt gat ggc ccc tgc aaa att ccg att gct tcc gtt gcg      2535
Tyr Ser Gly Ser Asp Gly Pro Cys Lys Ile Pro Ile Ala Ser Val Ala
525                 530                 535                 540

agc ctc aat gac atg acc ccc gtt ggg cgg ctg gtg aca gtg aac ccc      2583
Ser Leu Asn Asp Met Thr Pro Val Gly Arg Leu Val Thr Val Asn Pro
                545                 550                 555

ttc gtc gcg act tcc agt gcc agc tca aag gtg ctg gtc gag atg gaa      2631
Phe Val Ala Thr Ser Ser Ala Ser Ser Lys Val Leu Val Glu Met Glu
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ccc ccc ttc gga gac tcc tac atc gta gtt gga agg gga gac aag cag    2679
Pro Pro Phe Gly Asp Ser Tyr Ile Val Val Gly Arg Gly Asp Lys Gln
        575             580             585

atc aac cac cat tgg cac aaa gct gga agc acg ctg ggc aag gcc ttt    2727
Ile Asn His His Trp His Lys Ala Gly Ser Thr Leu Gly Lys Ala Phe
    590             595             600

tca aca act ttg aag gga gct caa aga ctg gca gcg ttg ggc gac aca    2775
Ser Thr Thr Leu Lys Gly Ala Gln Arg Leu Ala Ala Leu Gly Asp Thr
605             610             615             620

gcc tgg gac ttt ggc tct att gga ggg gtc ttc aac tcc ata gga aaa    2823
Ala Trp Asp Phe Gly Ser Ile Gly Gly Val Phe Asn Ser Ile Gly Lys
                625             630             635

gcc gtt cac caa gtg ttt ggt ggt gcc ttc aga aca ctc ttt ggg gga    2871
Ala Val His Gln Val Phe Gly Gly Ala Phe Arg Thr Leu Phe Gly Gly
            640             645             650

atg tct tgg atc aca caa ggg cta atg ggt gcc cta ctg ctc tgg atg    2919
Met Ser Trp Ile Thr Gln Gly Leu Met Gly Ala Leu Leu Leu Trp Met
        655             660             665

ggc gtc aac gca cga gac cga tca att gct ttg gcc ttc tta gcc aca    2967
Gly Val Asn Ala Arg Asp Arg Ser Ile Ala Leu Ala Phe Leu Ala Thr
        670             675             680

ggg ggt gtg ctc gtg ttc tta gcg acc aat gtg cat gct taattagttt    3016
Gly Gly Val Leu Val Phe Leu Ala Thr Asn Val His Ala
685             690             695
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gagcggccgc tcgagcatgc atctagaggg ccctattcta tagtgtcacc taaatgctag   3076

agctcgctga tcagcctcga ctgtgccttc tagttgccag ccatctgttg tttgcccctc   3136

ccccgtgcct tccttgaccc tggaaggtgc cactcccact gtcctttcct aataaaatga   3196

ggaaattgca tcgcattgtc tgagtaggtg tcattctatt ctggggggtg gggtggggca   3256

ggacagcaag ggggaggatt gggaagacaa tagcaggcat gctggggatg cggtgggctc   3316

tatggcttct gaggcggaaa gaaccagctg cattaatgaa tcggccaacg cgcggggaga   3376

ggcggtttgc gtattgggcg ctcttccgct cctcgctca ctgactcgct gcgctcggtc   3436

gttcggctgc ggcgagcggt atcagctcac tcaaaggcgg taatacggtt atccacagaa   3496

tcaggggata acgcaggaaa gaacatgtga gcaaaaggcc agcaaaaggc caggaaccgt   3556

aaaaaggccg cgttgctggc gtttttccat aggctccgcc ccccتgacga gcatcacaaa   3616

aatcgacgct caagtcagag gtggcgaaac ccgacaggac tataaagata ccaggcgttt   3676

cccctggaa gctccctcgt gcgctctcct gttccgaccc tgccgcttac cggatacctg   3736

tccgccttc tcccttcggg aagcgtggcg ctttctcata gctcacgctg taggtatctc   3796

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agttcggtgt aggtcgttcg ctccaagctg ggctgtgtgc acgaacccccc cgttcagccc    3856

gaccgctgcg ccttatccgg taactatcgt cttgagtcca acccggtaag acacgactta    3916

tcgccactgg cagcagccac tggtaacagg attagcagag cgaggtatgt aggcggtgct    3976

acagagttct tgaagtggtg gcctaactac ggctacacta gaagaacagt atttggtatc    4036

tgcgctctgc tgaagccagt taccttcgga aaaagagttg gtagctcttg atccggcaaa    4096

caaaccaccg ctggtagcgg tggtttttttt gtttgcaagc agcagattac gcgcagaaaa    4156

aaaggatctc aagaagatcc tttgatcttt tctacggggt ctgacgctca gtggaacgaa    4216

aactcacgtt aagggatttt ggtcatgaga ttatcaaaaa ggatcttcac ctagatcctt    4276

ttaaattaaa aatgaagttt taaatcaatc taaagtatat atgagtaaac ttggtctgac    4336

agttaccaat gcttaatcag tgaggcacct atctcagcga tctgtctatt tcgttcatcc    4396

atagttgcct gactccccgt cgtgtagata actacgatac gggagggctt accatctggc    4456

cccagtgctg caatgatacc gcgagaccca cgctcaccgg ctccagattt atcagcaata    4516

aaccagccag ccggaagggc cgagcgcaga agtggtcctg caactttatc cgcctccatc    4576

cagtctatta attgttgccg ggaagctaga gtaagtagtt cgccagttaa tagtttgcgc    4636

aacgttgttg ccattgctac aggcatcgtg gtgtcacgct cgtcgtttgg tatggcttca    4696

ttcagctccg gttcccaacg atcaaggcga gttacatgat cccccatgtt gtgcaaaaaa    4756

gcggttagct ccttcggtcc tccgatcgtt gtcagaagta agttggccgc agtgttatca    4816

ctcatggtta tggcagcact gcataattct cttactgtca tgccatccgt aagatgcttt    4876

tctgtgactg gtgagtactc aaccaagtca ttctgagaat agtgtatgcg gcgaccgagt    4936

tgctcttgcc cggcgtcaat acgggataat accgcgccac atagcagaac tttaaaagtg    4996

ctcatcattg gaaaacgttc ttcggggcga aaactctcaa ggatcttacc gctgttgaga    5056

tccagttcga tgtaacccac tcgtgcaccc aactgatctt cagcatcttt tactttcacc    5116

agcgtttctg ggtgagcaaa aacaggaagg caaaatgccg caaaaaaggg aataagggcg    5176

acacggaaat gttgaatact catactcttc cttttttcaat attattgaag catttatcag    5236

ggttattgtc tcatgagcgg atacatattt gaatgtattt agaaaaataa acaaataggg    5296

gttccgcgca catttccccg aaaagtgcca cctgacgt                            5334
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<210> 18
<211> 697
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note = synthetic construct

27

<400> 18

Met Gly Arg Lys Gln Asn Lys Arg Gly Gly Asn Glu Gly Ser Ile Met
1   5   10   15

Trp Leu Ala Ser Leu Ala Val Val Ile Ala Cys Ala Gly Ala Met Lys
            20   25   30

Leu Ser Asn Phe Gln Gly Lys Leu Leu Met Thr Ile Asn Asn Thr Asp
            35   40   45

Ile Ala Asp Val Ile Val Ile Pro Thr Ser Lys Gly Glu Asn Arg Cys
        50   55   60

Trp Val Arg Ala Ile Asp Val Gly Tyr Met Cys Glu Asp Thr Ile Thr
65   70   75   80

Tyr Glu Cys Pro Lys Leu Thr Met Gly Asn Asp Pro Glu Asp Val Asp
                85   90   95

Cys Trp Cys Asp Asn Gln Glu Val Tyr Val Gln Tyr Gly Arg Cys Thr
            100   105   110

Arg Thr Arg His Ser Lys Arg Ser Arg Arg Ser Val Ser Val Gln Thr
        115   120   125

His Gly Glu Ser Ser Leu Val Asn Lys Lys Glu Ala Trp Leu Asp Ser
        130   135   140

Thr Lys Ala Thr Arg Tyr Leu Met Lys Thr Glu Asn Trp Ile Ile Arg
145   150   155   160

Asn Pro Gly Tyr Ala Phe Leu Ala Ala Val Leu Gly Trp Met Leu Gly
                165   170   175

Ser Asn Asn Gly Gln Arg Val Val Phe Thr Ile Leu Leu Leu Leu Val
            180   185   190

Ala Pro Ala Tyr Ser Phe Asn Cys Leu Gly Met Gly Asn Arg Asp Phe
        195   200   205

Ile Glu Gly Ala Ser Gly Ala Thr Trp Val Asp Leu Val Leu Glu Gly
    210   215   220

Asp Ser Cys Leu Thr Ile Met Ala Asn Asp Lys Pro Thr Leu Asp Val

28

Arg Met Ile Asn Ile Glu Ala Ser Gln Leu Ala Glu Val Arg Ser Tyr
                245   250   255

Cys Tyr His Ala Ser Val Thr Asp Ile Ser Thr Val Ala Arg Cys Pro
                260   265   270

Thr Thr Gly Glu Ala His Asn Glu Lys Arg Ala Asp Ser Ser Tyr Val
                275   280   285

Cys Lys Gln Gly Phe Thr Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu
                290   295   300

Phe Gly Lys Gly Ser Ile Asp Thr Cys Ala Lys Phe Ser Cys Thr Ser
305   310   315   320

Lys Ala Ile Gly Arg Thr Ile Gln Pro Glu Asn Ile Lys Tyr Glu Val
                325   330   335

Gly Ile Phe Val His Gly Thr Thr Thr Ser Glu Asn His Gly Asn Tyr
                340   345   350

Ser Ala Gln Val Gly Ala Ser Gln Ala Ala Lys Phe Thr Val Thr Pro
                355   360   365

Asn Ala Pro Ser Ile Thr Leu Lys Leu Gly Asp Tyr Gly Glu Val Thr
                370   375   380

Leu Asp Cys Glu Pro Arg Ser Gly Leu Asn Thr Glu Ala Phe Tyr Val
385   390   395   400

Met Thr Val Gly Ser Lys Ser Phe Leu Val His Arg Glu Trp Phe His
                405   410   415

Asp Leu Ala Leu Pro Trp Thr Ser Pro Ser Ser Thr Ala Trp Arg Asn
                420   425   430

Arg Glu Leu Leu Met Glu Phe Glu Glu Ala His Ala Thr Lys Gln Ser
                435   440   445

Val Val Ala Leu Gly Ser Gln Glu Gly Gly Leu His Gln Ala Leu Ala
                450   455   460

Gly Ala Ile Val Val Glu Tyr Ser Ser Ser Val Lys Leu Thr Ser Gly

His Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Ala Leu Lys Gly Thr
              485   490   495

Thr Tyr Gly Met Cys Thr Glu Lys Phe Ser Phe Ala Lys Asn Pro Ala
              500   505   510

Asp Thr Gly His Gly Thr Val Val Ile Glu Leu Ser Tyr Ser Gly Ser
              515   520   525

Asp Gly Pro Cys Lys Ile Pro Ile Ala Ser Val Ala Ser Leu Asn Asp
              530   535   540

Met Thr Pro Val Gly Arg Leu Val Thr Val Asn Pro Phe Val Ala Thr
545   550   555   560

Ser Ser Ala Ser Ser Lys Val Leu Val Glu Met Glu Pro Pro Phe Gly
              565   570   575

Asp Ser Tyr Ile Val Val Gly Arg Gly Asp Lys Gln Ile Asn His His
              580   585   590

Trp His Lys Ala Gly Ser Thr Leu Gly Lys Ala Phe Ser Thr Thr Leu
              595   600   605

Lys Gly Ala Gln Arg Leu Ala Ala Leu Gly Asp Thr Ala Trp Asp Phe
              610   615   620

Gly Ser Ile Gly Gly Val Phe Asn Ser Ile Gly Lys Ala Val His Gln
625   630   635   640

Val Phe Gly Gly Ala Phe Arg Thr Leu Phe Gly Gly Met Ser Trp Ile
              645   650   655

Thr Gln Gly Leu Met Gly Ala Leu Leu Leu Trp Met Gly Val Asn Ala
              660   665   670

Arg Asp Arg Ser Ile Ala Leu Ala Phe Leu Ala Thr Gly Gly Val Leu
              675   680   685

Val Phe Leu Ala Thr Asn Val His Ala
690   695

<210> 19

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<211>  5283
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Description of artificial sequence; note = synthetic construct


<220>
<221>  CDS
<222>  (910)..(2964)

<400>  19
gacggatcgg gagatctccc gatcccctat ggtcgactct cagtacaatc tgctctgatg      60

ccgcatagtt aagccagtat ctgctccctg cttgtgtgtt ggaggtcgct gagtagtgcg     120

cgagcaaaat ttaagctaca caaggcaag gcttgaccga caattgcatg aagaatctgc      180

ttagggttag gcgttttgcg ctgcttcgcg atgtacgggc cagatatacg cgttgacatt     240

gattattgac tagttattaa tagtaatcaa ttacggggtc attagttcat agcccatata     300

tggagttccg cgttacataa cttacggtaa atggcccgcc tggctgaccg cccaacgacc     360

cccgcccatt gacgtcaata atgacgtatg ttcccatagt aacgccaata gggactttcc     420

attgacgtca atgggtggac tatttacggt aaactgccca cttggcagta catcaagtgt     480

atcatatgcc aagtacgccc cctattgacg tcaatgacgg taaatggccc gcctggcatt     540

atgcccagta catgacctta tgggactttc ctacttggca gtacatctac gtattagtca     600

tcgctattac catggtgatg cggttttggc agtacatcaa tgggcgtgga tagcggtttg     660

actcacgggg atttccaagt ctccacccca ttgacgtcaa tgggagtttg ttttggcacc     720

aaaatcaacg ggactttcca aaatgtcgta caactccgc cccattgacg caaatgggcg      780

gtaggcgtgt acggtgggag gtctatataa gcagagctct ctggctaact agagaaccca     840

ctgcttactg gcttatcgaa attaatacga ctcactatag ggagacccaa gcttggtacc     900

gccgccgcc atg ggc aag agg tcc gcc ggc tca atc atg tgg ctc gcg agc      951
          Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala Ser
           1               5                   10

ttg gca gtt gtc ata gct ggt aca agc gct acc acc atc cac cgg gac       999
Leu Ala Val Val Ile Ala Gly Thr Ser Ala Thr Thr Ile His Arg Asp
15                  20                  25                  30

agg gaa gga tac atg gtt atg cgg gcc agt gga agg gac gct gca agc      1047
Arg Glu Gly Tyr Met Val Met Arg Ala Ser Gly Arg Asp Ala Ala Ser
                35                  40                  45

cag gtc agg gta caa aac gga acg tgc gtc atc ctg gca aca gac atg      1095
Gln Val Arg Val Gln Asn Gly Thr Cys Val Ile Leu Ala Thr Asp Met
            50                  55                  60

gga gag tgg tgt gaa gat tca atc acc tac tct tgc gtc acg att gac      1143
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31

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Gly Glu Trp Cys Glu Asp Ser Ile Thr Tyr Ser Cys Val Thr Ile Asp
        65              70              75

cag gag gaa gaa ccc gtt gac gtg gac tgc ttc tgc cga ggt gtt gat          1191
Gln Glu Glu Glu Pro Val Asp Val Asp Cys Phe Cys Arg Gly Val Asp
        80              85              90

agg gtt aag tta gag tat gga cgc tgt gga agg caa gct gga tct agg          1239
Arg Val Lys Leu Glu Tyr Gly Arg Cys Gly Arg Gln Ala Gly Ser Arg
95              100             105             110

ggg aaa agg tct gtg gtc att cca aca cat gca caa aaa gac atg gtc          1287
Gly Lys Arg Ser Val Val Ile Pro Thr His Ala Gln Lys Asp Met Val
            115             120             125

ggg cga ggt cat gca tgg ctt aaa ggt gac aat att cga gat cat gtc          1335
Gly Arg Gly His Ala Trp Leu Lys Gly Asp Asn Ile Arg Asp His Val
            130             135             140

acc cga gtc gag ggc tgg atg tgg aag aac aag ctt cta act gcc gcc          1383
Thr Arg Val Glu Gly Trp Met Trp Lys Asn Lys Leu Leu Thr Ala Ala
            145             150             155

att gtg gcc ttg gct tgg ctc atg gtt gat agt tgg atg gcc aga gtg          1431
Ile Val Ala Leu Ala Trp Leu Met Val Asp Ser Trp Met Ala Arg Val
        160             165             170

act gtc atc ctc ttg gcg ttg agt cta ggg cca gtg tac gcc acg agg          1479
Thr Val Ile Leu Leu Ala Leu Ser Leu Gly Pro Val Tyr Ala Thr Arg
175             180             185             190

tgc acg cat ctt gag aac aga gat ttt gtg aca gga act caa ggg acc          1527
Cys Thr His Leu Glu Asn Arg Asp Phe Val Thr Gly Thr Gln Gly Thr
            195             200             205

acc aga gtg tcc cta gtt ttg gaa ctt gga ggc tgc gtg acc atc aca          1575
Thr Arg Val Ser Leu Val Leu Glu Leu Gly Gly Cys Val Thr Ile Thr
            210             215             220

gct gag ggc aag cca tcc att gat gta tgg ctc gaa gac att ttt cag          1623
Ala Glu Gly Lys Pro Ser Ile Asp Val Trp Leu Glu Asp Ile Phe Gln
        225             230             235

gaa agc ccg gct gaa acc aga gaa tac tgc ctg cac gcc aaa ttg acc          1671
Glu Ser Pro Ala Glu Thr Arg Glu Tyr Cys Leu His Ala Lys Leu Thr
        240             ·245            250

aac aca aaa gtg gag gct cgc tgt cca acc act gga ccg gcg aca ctt          1719
Asn Thr Lys Val Glu Ala Arg Cys Pro Thr Thr Gly Pro Ala Thr Leu
255             260             265             270

ccg gag gag cat cag gct aat atg gtg tgc aag aga gac caa agc gac          1767
Pro Glu Glu His Gln Ala Asn Met Val Cys Lys Arg Asp Gln Ser Asp
            275             280             285

cgt gga tgg gga aac cac tgc ggg ttt ttt ggg aag ggc agt ata gtg          1815
Arg Gly Trp Gly Asn His Cys Gly Phe Phe Gly Lys Gly Ser Ile Val
            290             295             300

gct tgt gca aag ttt gaa tgc gag gaa gca aaa aaa gct gtg ggc cac          1863
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32

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Ala Cys Ala Lys Phe Glu Cys Glu Glu Ala Lys Lys Ala Val Gly His
        305               310             315

gtc tat gac tcc aca aag atc acg tat gtt gtc aag gtt gag ccc cac    1911
Val Tyr Asp Ser Thr Lys Ile Thr Tyr Val Val Lys Val Glu Pro His
    320               325             330

aca ggg gat tac ttg gct gca aat gag acc aat tca aac agg aaa tca    1959
Thr Gly Asp Tyr Leu Ala Ala Asn Glu Thr Asn Ser Asn Arg Lys Ser
335               340             345             350

gca cag ttt acg gtg gca tcc gag aaa gtg atc ctg cgg ctc ggc gac    2007
Ala Gln Phe Thr Val Ala Ser Glu Lys Val Ile Leu Arg Leu Gly Asp
            355             360             365

tat gga gat gtg tcg ctg acg tgt aaa gtg gca agt ggg att gat gtc    2055
Tyr Gly Asp Val Ser Leu Thr Cys Lys Val Ala Ser Gly Ile Asp Val
            370             375             380

gcc caa act gtg gtg atg tca ctc gac agc agc aag gac cac ctg cct    2103
Ala Gln Thr Val Val Met Ser Leu Asp Ser Ser Lys Asp His Leu Pro
            385             390             395

tct gca tgg caa gtg cac cgt gac tgg ttt gag gac ttg gcg ctg ccc    2151
Ser Ala Trp Gln Val His Arg Asp Trp Phe Glu Asp Leu Ala Leu Pro
    400             405             410

tgg aaa cac aag gac aac caa gat tgg aac agt gtg gag aaa ctt gtg    2199
Trp Lys His Lys Asp Asn Gln Asp Trp Asn Ser Val Glu Lys Leu Val
415             420             425             430

gaa ttt gga cca cca cat gct gtg aaa atg gat gtt ttc aat ctg ggg    2247
Glu Phe Gly Pro Pro His Ala Val Lys Met Asp Val Phe Asn Leu Gly
            435             440             445

gac cag acg gct gtg ctg ctc aaa tca ctg gca gga gtt ccg ctg gcc    2295
Asp Gln Thr Ala Val Leu Leu Lys Ser Leu Ala Gly Val Pro Leu Ala
            450             455             460

agt gtg gag ggc cag aaa tac cac ctg aaa agc ggc cat gtt act tgt    2343
Ser Val Glu Gly Gln Lys Tyr His Leu Lys Ser Gly His Val Thr Cys
            465             470             475

gat gtg gga ctg gaa aag ctg aaa ctg aaa ggc aca acc tac tcc atg    2391
Asp Val Gly Leu Glu Lys Leu Lys Leu Lys Gly Thr Thr Tyr Ser Met
    480             485             490

tgt gac aaa gca aag ttc aaa tgg aag aga gtt cct gtg gac agc ggc    2439
Cys Asp Lys Ala Lys Phe Lys Trp Lys Arg Val Pro Val Asp Ser Gly
495             500             505             510

cat gac aca gta gtc atg gag gta tca tac aca gga agc gac aag cca    2487
His Asp Thr Val Val Met Glu Val Ser Tyr Thr Gly Ser Asp Lys Pro
            515             520             525

tgt cgg atc ccg gtg cgg gct gtg gca cat ggt gtc cca gcg gtt aat    2535
Cys Arg Ile Pro Val Arg Ala Val Ala His Gly Val Pro Ala Val Asn
            530             535             540

gta gcc atg ctc ata acc ccc aat cca acc att gaa aca aat ggt ggc    2583
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        Val Ala Met Leu Ile Thr Pro Asn Pro Thr Ile Glu Thr Asn Gly Gly
              545                 550                 555

gga ttc ata gaa atg cag ctg cca cca ggg gat aac atc atc tat gtg      2631
Gly Phe Ile Glu Met Gln Leu Pro Pro Gly Asp Asn Ile Ile Tyr Val
        560                 565                 570

gga gac ctt agc cag cag tgg ttt cag aaa ggc agt acc att ggt aga      2679
Gly Asp Leu Ser Gln Gln Trp Phe Gln Lys Gly Ser Thr Ile Gly Arg
575                 580                 585                 590

atg ttt gaa aaa acc cgc agg gga ttg gaa agg ctc tct gtg gtt gga      2727
Met Phe Glu Lys Thr Arg Arg Gly Leu Glu Arg Leu Ser Val Val Gly
                595                 600                 605

gaa cat gca tgg gac ttt ggc tca gta ggc ggg gta ctg tct tct gtg      2775
Glu His Ala Trp Asp Phe Gly Ser Val Gly Gly Val Leu Ser Ser Val
            610                 615                 620

ggg aag gca atc cac acg gtg ctg ggg gga gct ttc aac acc ctt ttt      2823
Gly Lys Ala Ile His Thr Val Leu Gly Gly Ala Phe Asn Thr Leu Phe
        625                 630                 635

ggg ggg gtt gga ttc atc cct aag atg ctg ctg ggg gtt gct ctg gtc      2871
Gly Gly Val Gly Phe Ile Pro Lys Met Leu Leu Gly Val Ala Leu Val
        640                 645                 650

tgg ttg gga cta aat gcc agg aat cca acg atg tcc atg acg ttt ctt      2919
Trp Leu Gly Leu Asn Ala Arg Asn Pro Thr Met Ser Met Thr Phe Leu
655                 660                 665                 670

gct gtg ggg gct ttg aca ctg atg atg aca atg gga gtt ggg gca          2964
Ala Val Gly Ala Leu Thr Leu Met Met Thr Met Gly Val Gly Ala
                675                 680                 685

tgagcggccg ctcgagcatg catctagagg gccctattct atagtgtcac ctaaatgcta    3024

gagctcgctg atcagcctcg actgtgcctt ctagttgcca gccatctgtt gtttgcccct    3084

cccccgtgcc ttccttgacc ctggaaggtg ccactcccac tgtcctttcc taataaaatg    3144

aggaaattgc atcgcattgt ctgagtaggt gtcattctat tctggggggt ggggtggggc    3204

aggacagcaa gggggaggat tgggaagaca atagcaggca tgctggggat gcggtgggct    3264

ctatggcttc tgaggcggaa agaacagctg cattaatgaa tcggccaacg cgcggggaga    3324

ggcggtttgc gtattgggcg ctcttccgct tcctcgctca ctgactcgct gcgctcggtc    3384

gttcggctgc ggcgagcggt atcagctcac tcaaaggcgg taatacggtt atccacagaa    3444

tcaggggata acgcaggaaa gaacatgtga gcaaaaggcc agcaaaaggc aggaaccgt     3504

aaaaaggccg cgttgctggc gtttttccat aggctccgcc cccctgacga gcatcacaaa    3564

aatcgacgct caagtcagag gtggcgaaac ccgacaggac tataaagata ccaggcgttt    3624

cccccctggaa gctccctcgt gcgctctcct gttccgaccc tgccgcttac cggatacctg    3684

tccgcctttc tcccttcggg aagcgtggcg ctttctcaat gctcacgctg taggtatctc    3744
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34

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agttcggtgt aggtcgttcg ctccaagctg ggctgtgtgc acgaacccccc cgttcagccc    3804

gaccgctgcg ccttatccgg taactatcgt cttgagtcca acccggtaag acacgactta    3864

tcgccactgg cagcagccac tggtaacagg attagcagag cgaggtatgt aggcggtgct    3924

acagagttct tgaagtggtg gcctaactac ggctacacta gaaggacagt atttggtatc    3984

tgcgctctgc tgaagccagt taccttcgga aaaagagttg gtagctcttg atccggcaaa    4044

caaaccaccg ctggtagcgg tggttttttt gtttgcaagc agcagattac gcgcagaaaa    4104

aaaggatctc aagaagatcc tttgatcttt tctacggggt ctgacgctca gtggaacgaa    4164

aactcacgtt aagggatttt ggtcatgaga ttatcaaaaa ggatcttcac ctagatcctt    4224

ttaaattaaa aatgaagttt taaatcaatc taaagtatat atgagtaaac ttggtctgac    4284

agttaccaat gcttaatcag tgaggcacct atctcagcga tctgtctatt tcgttcatcc    4344

atagttgcct gactccccgt cgtgtagata actacgatac gggagggctt accatctggc    4404

cccagtgctg caatgatacc gcgagaccca cgctcaccgg ctccagattt atcagcaata    4464

aaccagccag ccggaagggc cgagcgcaga agtggtcctg caactttatc cgcctccatc    4524

cagtctatta attgttgccg ggaagctaga gtaagtagtt cgccagttaa tagtttgcgc    4584

aacgttgttg ccattgctac aggcatcgtg gtgtcacgct cgtcgtttgg tatggcttca    4644

ttcagctccg gttcccaacg atcaaggcga gttacatgat cccccatgtt gtgcaaaaaa    4704

gcggttagct ccttcggtcc tccgatcgtt gtcagaagta agttggccgc agtgttatca    4764

ctcatggtta tggcagcact gcataattct cttactgtca tgccatccgt aagatgcttt    4824

tctgtgactg gtgagtactc aaccaagtca ttctgagaat agtgtatgcg gcgaccgagt    4884

tgctcttgcc cggcgtcaat acgggataat accgcgccac atagcagaac tttaaaagtg    4944

ctcatcattg gaaaacgttc ttcggggcga aaactctcaa ggatcttacc gctgttgaga    5004

tccagttcga tgtaacccac tcgtgcaccc aactgatctt cagcatcttt tactttcacc    5064

agcgtttctg ggtgagcaaa aacaggaagg caaaatgccg caaaaaaggg aataagggcg    5124

acacggaaat gttgaatact catactcttc ctttttcaat attattgaag catttatcag    5184

ggttattgtc tcatgagcgg atacatattt gaatgtattt agaaaaataa acaaataggg    5244

gttccgcgca catttccccg aaaagtgcca cctgacgtc                           5283
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<210>   20
<211>   685
<212>   PRT
<213>   Artificial Sequence

<220>

35

<223> Description of artificial sequence; note = synthetic construct

<400> 20

Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala Ser Leu Ala
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Val Val Ile Ala Gly Thr Ser Ala Thr Thr Ile His Arg Asp Arg Glu
            20   25   30

Gly Tyr Met Val Met Arg Ala Ser Gly Arg Asp Ala Ala Ser Gln Val
            35   40   45

Arg Val Gln Asn Gly Thr Cys Val Ile Leu Ala Thr Asp Met Gly Glu
    50   55   60

Trp Cys Glu Asp Ser Ile Thr Tyr Ser Cys Val Thr Ile Asp Gln Glu
65   70   75   80

Glu Glu Pro Val Asp Val Asp Cys Phe Cys Arg Gly Val Asp Arg Val
            85   90   95

Lys Leu Glu Tyr Gly Arg Cys Gly Arg Gln Ala Gly Ser Arg Gly Lys
            100   105   110

Arg Ser Val Val Ile Pro Thr His Ala Gln Lys Asp Met Val Gly Arg
        115   120   125

Gly His Ala Trp Leu Lys Gly Asp Asn Ile Arg Asp His Val Thr Arg
    130   135   140

Val Glu Gly Trp Met Trp Lys Asn Lys Leu Leu Thr Ala Ala Ile Val
145   150   155   160

Ala Leu Ala Trp Leu Met Val Asp Ser Trp Met Ala Arg Val Thr Val
            165   170   175

Ile Leu Leu Ala Leu Ser Leu Gly Pro Val Tyr Ala Thr Arg Cys Thr
            180   185   190

His Leu Glu Asn Arg Asp Phe Val Thr Gly Thr Gln Gly Thr Thr Arg
        195   200   205

Val Ser Leu Val Leu Glu Leu Gly Gly Cys Val Thr Ile Thr Ala Glu
    210   215   220

36

Gly Lys Pro Ser Ile Asp Val Trp Leu Glu Asp Ile Phe Gln Glu Ser
225   230   235   240

Pro Ala Glu Thr Arg Glu Tyr Cys Leu His Ala Lys Leu Thr Asn Thr
                245   250   255

Lys Val Glu Ala Arg Cys Pro Thr Thr Gly Pro Ala Thr Leu Pro Glu
            260   265   270

Glu His Gln Ala Asn Met Val Cys Lys Arg Asp Gln Ser Asp Arg Gly
        275   280   285

Trp Gly Asn His Cys Gly Phe Phe Gly Lys Gly Ser Ile Val Ala Cys
    290   295   300

Ala Lys Phe Glu Cys Glu Glu Ala Lys Lys Ala Val Gly His Val Tyr
305   310   315   320

Asp Ser Thr Lys Ile Thr Tyr Val Val Lys Val Glu Pro His Thr Gly
            325   330   335

Asp Tyr Leu Ala Ala Asn Glu Thr Asn Ser Asn Arg Lys Ser Ala Gln
            340   345   350

Phe Thr Val Ala Ser Glu Lys Val Ile Leu Arg Leu Gly Asp Tyr Gly
        355   360   365

Asp Val Ser Leu Thr Cys Lys Val Ala Ser Gly Ile Asp Val Ala Gln
    370   375   380

Thr Val Val Met Ser Leu Asp Ser Ser Lys Asp His Leu Pro Ser Ala
385   390   395   400

Trp Gln Val His Arg Asp Trp Phe Glu Asp Leu Ala Leu Pro Trp Lys
            405   410   415

His Lys Asp Asn Gln Asp Trp Asn Ser Val Glu Lys Leu Val Glu Phe
            420   425   430

Gly Pro Pro His Ala Val Lys Met Asp Val Phe Asn Leu Gly Asp Gln
        435   440   445

Thr Ala Val Leu Leu Lys Ser Leu Ala Gly Val Pro Leu Ala Ser Val
    450   455   460

37

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Glu Gly Gln Lys Tyr His Leu Lys Ser Gly His Val Thr Cys Asp Val
465                 470             475             480


Gly Leu Glu Lys Leu Lys Leu Lys Gly Thr Thr Tyr Ser Met Cys Asp
                485             490             495


Lys Ala Lys Phe Lys Trp Lys Arg Val Pro Val Asp Ser Gly His Asp
            500             505             510


Thr Val Val Met Glu Val Ser Tyr Thr Gly Ser Asp Lys Pro Cys Arg
        515             520             525


Ile Pro Val Arg Ala Val Ala His Gly Val Pro Ala Val Asn Val Ala
    530             535             540


Met Leu Ile Thr Pro Asn Pro Thr Ile Glu Thr Asn Gly Gly Gly Phe
545             550             555             560


Ile Glu Met Gln Leu Pro Pro Gly Asp Asn Ile Ile Tyr Val Gly Asp
            565             570             575


Leu Ser Gln Gln Trp Phe Gln Lys Gly Ser Thr Ile Gly Arg Met Phe
            580             585             590


Glu Lys Thr Arg Arg Gly Leu Glu Arg Leu Ser Val Val Gly Glu His
        595             600             605


Ala Trp Asp Phe Gly Ser Val Gly Gly Val Leu Ser Ser Val Gly Lys
    610             615             620


Ala Ile His Thr Val Leu Gly Gly Ala Phe Asn Thr Leu Phe Gly Gly
625             630             635             640


Val Gly Phe Ile Pro Lys Met Leu Leu Gly Val Ala Leu Val Trp Leu
            645             650             655


Gly Leu Asn Ala Arg Asn Pro Thr Met Ser Met Thr Phe Leu Ala Val
            660             665             670


Gly Ala Leu Thr Leu Met Met Thr Met Gly Val Gly Ala
        675             680             685


<210>  21
<211>  5304
<212>  DNA
<213>  Artificial Sequence

                        38
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<400> 21

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ccgcatagtt aagccagtat ctgctccctg cttgtgtgtt ggaggtcgct gagtagtgcg     120

cgagcaaaat ttaagctaca caaggcaag gcttgaccga caattgcatg aagaatctgc      180

ttagggttag gcgttttgcg ctgcttcgcg atgtacgggc cagatatacg cgttgacatt     240

gattattgac tagttattaa tagtaatcaa ttacggggtc attagttcat agcccatata     300

tggagttccg cgttacataa cttacggtaa atggcccgcc tggctgaccg cccaacgacc     360

cccgcccatt gacgtcaata atgacgtatg ttcccatagt aacgccaata gggactttcc     420

attgacgtca atgggtggac tatttacggt aaactgccca cttggcagta catcaagtgt     480

atcatatgcc aagtacgccc cctattgacg tcaatgacgg taaatggccc gcctggcatt     540

atgcccagta catgacctta tgggactttc ctacttggca gtacatctac gtattagtca     600

tcgctattac catggtgatg cggttttggc agtacatcaa tgggcgtgga tagcggtttg     660

actcacgggg atttccaagt ctccacccca ttgacgtcaa tgggagtttg ttttggcacc     720

aaaatcaacg ggactttcca aaatgtcgta acaactccgc cccattgacg caaatgggcg     780

gtaggcgtgt acggtgggag gtctatataa gcagagctct ctggctaact agagaaccca     840

ctgcttactg gcttatcgaa attaatacga ctcactatag ggagacccaa gcttggtacc     900
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gccgccgcc atg ggc aag agg tcc gcc ggc tca atc atg tgg ctc gcg agc      951
          Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala Ser
          1                5                   10

ttg gca gtt gtc ata gct ggt aca agc gct ttg cag tta tca acc tat       999
Leu Ala Val Val Ile Ala Gly Thr Ser Ala Leu Gln Leu Ser Thr Tyr
15                  20                  25                  30

cag ggg aaa gtg tta atg tca atc aac aag act gac gct caa agc gcc      1047
Gln Gly Lys Val Leu Met Ser Ile Asn Lys Thr Asp Ala Gln Ser Ala
                35                  40                  45

ata aac att cct agt gcc aac gga gca aac act tgc att gtg agg gct      1095
Ile Asn Ile Pro Ser Ala Asn Gly Ala Asn Thr Cys Ile Val Arg Ala
                50                  55                  60

cta gat gtg ggg gtc atg tgc aaa gat gac atc aca tac ctg tgc cca      1143
Leu Asp Val Gly Val Met Cys Lys Asp Asp Ile Thr Tyr Leu Cys Pro
          65                  70                  75
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39

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gtg ctt tca gcg gga aat gat ccc gag gac att gac tgt tgg tgt gac        1191
Val Leu Ser Ala Gly Asn Asp Pro Glu Asp Ile Asp Cys Trp Cys Asp
    80                  85                  90

gtc gaa gag gtg tgg gtg cac tac ggc aga tgc acg cgc atg gga cat        1239
Val Glu Glu Val Trp Val His Tyr Gly Arg Cys Thr Arg Met Gly His
95                  100                 105                 110

tcg agg cgt agc cga cgg tca atc tct gtg cag cat cat gga gat tcc        1287
Ser Arg Arg Ser Arg Arg Ser Ile Ser Val Gln His His Gly Asp Ser
                115                 120                 125

aca ctg gca aca aag aac acg cca tgg ttg gac acc gtg aaa acc acc        1335
Thr Leu Ala Thr Lys Asn Thr Pro Trp Leu Asp Thr Val Lys Thr Thr
                130                 135                 140

aaa tac ttg aca aaa gta gaa aac tgg gtt ttg cgc aat cct gga tat        1383
Lys Tyr Leu Thr Lys Val Glu Asn Trp Val Leu Arg Asn Pro Gly Tyr
            145                 150                 155

gcc cta gtt gcg ctg gcg att gga tgg atg ctc ggt agc aac aac aca        1431
Ala Leu Val Ala Leu Ala Ile Gly Trp Met Leu Gly Ser Asn Asn Thr
    160                 165                 170

cag aga gtg gtt ttt gtg atc atg ctg atg ctg att gct ccg gca tac        1479
Gln Arg Val Val Phe Val Ile Met Leu Met Leu Ile Ala Pro Ala Tyr
175                 180                 185                 190

agc ttc aac tgt ctg gga aca tca aac agg gac ttt gtc gag gga gcc        1527
Ser Phe Asn Cys Leu Gly Thr Ser Asn Arg Asp Phe Val Glu Gly Ala
                195                 200                 205

agt ggg gca aca tgg att gac ttg gta ctt gaa ggg gga agc tgt gtc        1575
Ser Gly Ala Thr Trp Ile Asp Leu Val Leu Glu Gly Gly Ser Cys Val
                210                 215                 220

aca gtg atg gca cca gag aaa cca aca ctg gac ttc aaa gtg atg aag        1623
Thr Val Met Ala Pro Glu Lys Pro Thr Leu Asp Phe Lys Val Met Lys
            225                 230                 235

atg gag gct acc gag tta gcc act gtg cgt gag tat tgt tac gaa gca        1671
Met Glu Ala Thr Glu Leu Ala Thr Val Arg Glu Tyr Cys Tyr Glu Ala
    240                 245                 250

acc ttg gac acg ctg tca aca gtg gca agg tgc ccc aca aca gga gaa        1719
Thr Leu Asp Thr Leu Ser Thr Val Ala Arg Cys Pro Thr Thr Gly Glu
255                 260                 265                 270

gct cac aac acc aaa agg agt gac cca aca ttt gtc tgc aaa aga gat        1767
Ala His Asn Thr Lys Arg Ser Asp Pro Thr Phe Val Cys Lys Arg Asp
                275                 280                 285

gtt gtg gac cgc gga tgg ggt aac gga tgt ggt ctg ttt gga aaa ggg        1815
Val Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly
                290                 295                 300

agc att gac aca tgc gct aag ttc aca tgc aaa aac aag gca aca ggg        1863
Ser Ile Asp Thr Cys Ala Lys Phe Thr Cys Lys Asn Lys Ala Thr Gly
            305                 310                 315
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40

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aag acg atc ttg aga gaa aac atc aag tat gag gtt gca atc ttt gtg      1911
Lys Thr Ile Leu Arg Glu Asn Ile Lys Tyr Glu Val Ala Ile Phe Val
    320             325             330

cat ggt tca acg gac tct acg tca cat ggc aat tac tct gag cag att      1959
His Gly Ser Thr Asp Ser Thr Ser His Gly Asn Tyr Ser Glu Gln Ile
335             340             345             350

gga aaa aac caa gcg gct aga ttc acc ata agc ccg caa gca ccg tcc      2007
Gly Lys Asn Gln Ala Ala Arg Phe Thr Ile Ser Pro Gln Ala Pro Ser
            355             360             365

ttt acg gcc aac atg ggc gag tat gga aca gtt acc att gat tgt gaa      2055
Phe Thr Ala Asn Met Gly Glu Tyr Gly Thr Val Thr Ile Asp Cys Glu
            370             375             380

gca aga tca gga atc aac acg gag gat tat tat gtt ttc act gtc aag      2103
Ala Arg Ser Gly Ile Asn Thr Glu Asp Tyr Tyr Val Phe Thr Val Lys
            385             390             395

gag aag tca tgg cta gtg aac agg gac tgg ttt cac gac ttg aac ctt      2151
Glu Lys Ser Trp Leu Val Asn Arg Asp Trp Phe His Asp Leu Asn Leu
            400             405             410

cca tgg acg agc cct gcc aca act gat tgg cgc aac aga gaa aca ctg      2199
Pro Trp Thr Ser Pro Ala Thr Thr Asp Trp Arg Asn Arg Glu Thr Leu
415             420             425             430

gtg gaa ttt gag gaa ccg cat gcc acc aag caa act gta gta gcc cta      2247
Val Glu Phe Glu Glu Pro His Ala Thr Lys Gln Thr Val Val Ala Leu
            435             440             445

gga tcg caa gaa ggt gcc ctg cac aca gca ttg gct gga gcc att cca      2295
Gly Ser Gln Glu Gly Ala Leu His Thr Ala Leu Ala Gly Ala Ile Pro
            450             455             460

gcc act gtt agc agc tca acc cta acc ttg caa tca ggg cat ttg aaa      2343
Ala Thr Val Ser Ser Ser Thr Leu Thr Leu Gln Ser Gly His Leu Lys
            465             470             475

tgc aga gct aag ctt gac aag gtc aaa atc aag gga acg aca tat ggc      2391
Cys Arg Ala Lys Leu Asp Lys Val Lys Ile Lys Gly Thr Thr Tyr Gly
    480             485             490

atg tgt gac tct gcc ttc acc ttc agc aag aac cca act gac aca ggg      2439
Met Cys Asp Ser Ala Phe Thr Phe Ser Lys Asn Pro Thr Asp Thr Gly
495             500             505             510

cac ggg aca gtg att gtg gaa ctg cag tat act gga agc aac gga ccc      2487
His Gly Thr Val Ile Val Glu Leu Gln Tyr Thr Gly Ser Asn Gly Pro
            515             520             525

tgc cga gtt ccc atc tcc gtg act gca aac ctc atg gat ttg aca ccg      2535
Cys Arg Val Pro Ile Ser Val Thr Ala Asn Leu Met Asp Leu Thr Pro
            530             535             540

gtt gga aga ttg gtc acg gtc aat ccc ttt ata agc aca ggg gga gcg      2583
Val Gly Arg Leu Val Thr Val Asn Pro Phe Ile Ser Thr Gly Gly Ala
            545             550             555
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41

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aac aac aag gtc atg atc gaa gtt gaa cca ccc ttt ggc gat tct tac     2631
Asn Asn Lys Val Met Ile Glu Val Glu Pro Pro Phe Gly Asp Ser Tyr
        560             565             570

atc gtc gtc gga aga ggc acc acc cag att aac tac cac tgg cac aaa     2679
Ile Val Val Gly Arg Gly Thr Thr Gln Ile Asn Tyr His Trp His Lys
575             580             585             590

gag gga agc agc att ggg aag gct ttg gcg acc aca tgg aaa gga gcc     2727
Glu Gly Ser Ser Ile Gly Lys Ala Leu Ala Thr Thr Trp Lys Gly Ala
            595             600             605

caa cgg cta gcc gtc tta ggg gac aca gcg tgg gac ttt gga tct att     2775
Gln Arg Leu Ala Val Leu Gly Asp Thr Ala Trp Asp Phe Gly Ser Ile
            610             615             620

gga gga gtt ttc aat tca att ggc aaa gct gtc cac caa gtt ttc gga     2823
Gly Gly Val Phe Asn Ser Ile Gly Lys Ala Val His Gln Val Phe Gly
            625             630             635

gga gcg ttc agg act ctg ttc ggg gga atg tcc tgg atc aca cag ggg     2871
Gly Ala Phe Arg Thr Leu Phe Gly Gly Met Ser Trp Ile Thr Gln Gly
        640             645             650

cta ctt gga gct ctt ctc ctg tgg atg ggg ttg cag gcc cgc gac agg     2919
Leu Leu Gly Ala Leu Leu Leu Trp Met Gly Leu Gln Ala Arg Asp Arg
655             660             665             670

agc atc tcg ctg act cta ctg gct gtc gga ggg att ctc atc ttt ctg     2967
Ser Ile Ser Leu Thr Leu Leu Ala Val Gly Gly Ile Leu Ile Phe Leu
            675             680             685

gca acc agc gtg caa gcc tgagcggccg ctcgagcatg catctagagg            3015
Ala Thr Ser Val Gln Ala
            690

gccctattct atagtgtcac ctaaatgcta gagctcgctg atcagcctcg actgtgcctt     3075

ctagttgcca gccatctgtt gtttgcccct cccccgtgcc ttccttgacc ctggaaggtg     3135

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gtcattctat tctggggggt ggggtggggc aggacagcaa ggggggaggat tgggaagaca     3255

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cattaatgaa tcggccaacg cgcggggaga ggcggtttgc gtattgggcg ctcttccgct     3375

tcctcgctca ctgactcgct gcgctcggtc gttcggctgc ggcgagcggt atcagctcac     3435

tcaaaggcgg taatacggtt atccacagaa tcaggggata acgcaggaaa gaacatgtga     3495

gcaaaaggcc agcaaaaggc caggaaccgt aaaaaggccg cgttgctggc gtttttccat     3555

aggctccgcc cccctgacga gcatcacaaa aatcgacgct caagtcagag gtggcgaaac     3615

ccgacaggac tataaagata ccaggcgttt ccccctggaa gctccctcgt gcgctctcct     3675

gttccgaccc tgccgcttac cggatacctg tccgcctttc tcccttcggg aagcgtggcg     3735
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42

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ctttctcaat gctcacgctg taggtatctc agttcggtgt aggtcgttcg ctccaagctg    3795

ggctgtgtgc acgaaccccc cgttcagccc gaccgctgcg ccttatccgg taactatcgt    3855

cttgagtcca acccggtaag acacgactta tcgccactgg cagcagccac tggtaacagg    3915

attagcagag cgaggtatgt aggcggtgct acagagttct tgaagtggtg gcctaactac    3975

ggctacacta gaaggacagt atttggtatc tgcgctctgc tgaagccagt taccttcgga    4035

aaaagagttg gtagctcttg atccggcaaa caaaccaccg ctggtagcgg tggttttttt    4095

gtttgcaagc agcagattac gcgcagaaaa aaaggatctc aagaagatcc tttgatcttt    4155

tctacggggt ctgacgctca gtggaacgaa aactcacgtt aagggatttt ggtcatgaga    4215

ttatcaaaaa ggatcttcac ctagatcctt ttaaattaaa aatgaagttt taaatcaatc    4275

taaagtatat atgagtaaac ttggtctgac agttaccaat gcttaatcag tgaggcacct    4335

atctcagcga tctgtctatt tcgttcatcc atagttgcct gactccccgt cgtgtagata    4395

actacgatac gggagggctt accatctggc cccagtgctg caatgatacc gcgagaccca    4455

cgctcaccgg ctccagattt atcagcaata aaccagccag ccggaagggc cgagcgcaga    4515

agtggtcctg caactttatc cgcctccatc cagtctatta attgttgccg ggaagctaga    4575

gtaagtagtt cgccagttaa tagtttgcgc aacgttgttg ccattgctac aggcatcgtg    4635

gtgtcacgct cgtcgtttgg tatggcttca ttcagctccg gttcccaacg atcaaggcga    4695

gttacatgat cccccatgtt gtgcaaaaaa gcggttagct ccttcggtcc tccgatcgtt    4755

gtcagaagta agttggccgc agtgttatca ctcatggtta tggcagcact gcataattct    4815

cttactgtca tgccatccgt aagatgcttt tctgtgactg gtgagtactc aaccaagtca    4875

ttctgagaat agtgtatgcg gcgaccgagt tgctcttgcc cggcgtcaat acgggataat    4935

accgcgccac atagcagaac tttaaaagtg ctcatcattg gaaaacgttc ttcggggcga    4995

aaactctcaa ggatcttacc gctgttgaga tccagttcga tgtaacccac tcgtgcaccc    5055

aactgatctt cagcatcttt tactttcacc agcgtttctg ggtgagcaaa aacaggaagg    5115

caaaatgccg caaaaaaggg aataagggcg acacggaaat gttgaatact catactcttc    5175

cttttttcaat attattgaag catttatcag ggttattgtc tcatgagcgg atacatattt    5235

gaatgtattt agaaaaataa acaaataggg gttccgcgca catttccccg aaaagtgcca    5295

cctgacgtc                                                            5304
```

<220>
<223> Description of artificial sequence; note = synthetic construct

<400> 22

Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala Ser Leu Ala
1   5   10   15

Val Val Ile Ala Gly Thr Ser Ala Leu Gln Leu Ser Thr Tyr Gln Gly
            20   25   30

Lys Val Leu Met Ser Ile Asn Lys Thr Asp Ala Gln Ser Ala Ile Asn
            35   40   45

Ile Pro Ser Ala Asn Gly Ala Asn Thr Cys Ile Val Arg Ala Leu Asp
        50   55   60

Val Gly Val Met Cys Lys Asp Asp Ile Thr Tyr Leu Cys Pro Val Leu
65   70   75   80

Ser Ala Gly Asn Asp Pro Glu Asp Ile Asp Cys Trp Cys Asp Val Glu
                85   90   95

Glu Val Trp Val His Tyr Gly Arg Cys Thr Arg Met Gly His Ser Arg
            100   105   110

Arg Ser Arg Arg Ser Ile Ser Val Gln His His Gly Asp Ser Thr Leu
            115   120   125

Ala Thr Lys Asn Thr Pro Trp Leu Asp Thr Val Lys Thr Thr Lys Tyr
        130   135   140

Leu Thr Lys Val Glu Asn Trp Val Leu Arg Asn Pro Gly Tyr Ala Leu
145   150   155   160

Val Ala Leu Ala Ile Gly Trp Met Leu Gly Ser Asn Asn Thr Gln Arg
            165   170   175

Val Val Phe Val Ile Met Leu Met Leu Ile Ala Pro Ala Tyr Ser Phe
            180   185   190

Asn Cys Leu Gly Thr Ser Asn Arg Asp Phe Val Glu Gly Ala Ser Gly
        195   200   205

Ala Thr Trp Ile Asp Leu Val Leu Glu Gly Gly Ser Cys Val Thr Val
    210   215   220

44

```
Met Ala Pro Glu Lys Pro Thr Leu Asp Phe Lys Val Met Lys Met Glu
225             230             235             240

Ala Thr Glu Leu Ala Thr Val Arg Glu Tyr Cys Tyr Glu Ala Thr Leu
            245             250             255

Asp Thr Leu Ser Thr Val Ala Arg Cys Pro Thr Thr Gly Glu Ala His
            260             265             270

Asn Thr Lys Arg Ser Asp Pro Thr Phe Val Cys Lys Arg Asp Val Val
            275             280             285

Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser Ile
    290             295             300

Asp Thr Cys Ala Lys Phe Thr Cys Lys Asn Lys Ala Thr Gly Lys Thr
305             310             315             320

Ile Leu Arg Glu Asn Ile Lys Tyr Glu Val Ala Ile Phe Val His Gly
            325             330             335

Ser Thr Asp Ser Thr Ser His Gly Asn Tyr Ser Glu Gln Ile Gly Lys
            340             345             350

Asn Gln Ala Ala Arg Phe Thr Ile Ser Pro Gln Ala Pro Ser Phe Thr
            355             360             365

Ala Asn Met Gly Glu Tyr Gly Thr Val Thr Ile Asp Cys Glu Ala Arg
    370             375             380

Ser Gly Ile Asn Thr Glu Asp Tyr Tyr Val Phe Thr Val Lys Glu Lys
385             390             395             400

Ser Trp Leu Val Asn Arg Asp Trp Phe His Asp Leu Asn Leu Pro Trp
            405             410             415

Thr Ser Pro Ala Thr Thr Asp Trp Arg Asn Arg Glu Thr Leu Val Glu
            420             425             430

Phe Glu Glu Pro His Ala Thr Lys Gln Thr Val Val Ala Leu Gly Ser
    435             440             445

Gln Glu Gly Ala Leu His Thr Ala Leu Ala Gly Ala Ile Pro Ala Thr
    450             455             460
```

```
Val Ser Ser Ser Thr Leu Thr Leu Gln Ser Gly His Leu Lys Cys Arg
465             470             475             480


Ala Lys Leu Asp Lys Val Lys Ile Lys Gly Thr Thr Tyr Gly Met Cys
                485             490             495


Asp Ser Ala Phe Thr Phe Ser Lys Asn Pro Thr Asp Thr Gly His Gly
            500             505             510


Thr Val Ile Val Glu Leu Gln Tyr Thr Gly Ser Asn Gly Pro Cys Arg
            515             520             525


Val Pro Ile Ser Val Thr Ala Asn Leu Met Asp Leu Thr Pro Val Gly
    530             535             540


Arg Leu Val Thr Val Asn Pro Phe Ile Ser Thr Gly Gly Ala Asn Asn
545             550             555             560


Lys Val Met Ile Glu Val Glu Pro Pro Phe Gly Asp Ser Tyr Ile Val
            565             570             575


Val Gly Arg Gly Thr Thr Gln Ile Asn Tyr His Trp His Lys Glu Gly
            580             585             590


Ser Ser Ile Gly Lys Ala Leu Ala Thr Thr Trp Lys Gly Ala Gln Arg
        595             600             605


Leu Ala Val Leu Gly Asp Thr Ala Trp Asp Phe Gly Ser Ile Gly Gly
    610             615             620


Val Phe Asn Ser Ile Gly Lys Ala Val His Gln Val Phe Gly Gly Ala
625             630             635             640


Phe Arg Thr Leu Phe Gly Gly Met Ser Trp Ile Thr Gln Gly Leu Leu
            645             650             655


Gly Ala Leu Leu Leu Trp Met Gly Leu Gln Ala Arg Asp Arg Ser Ile
        660             665             670


Ser Leu Thr Leu Leu Ala Val Gly Gly Ile Leu Ile Phe Leu Ala Thr
        675             680             685


Ser Val Gln Ala
    690
```

```
<210>   23
<211>   5271
<212>   DNA
<213>   Artificial Sequence

<220>
<223>   Description of artificial sequence; note = synthetic construct


<220>
<221>   CDS
<222>   (910)..(2952)

<400>   23
gacggatcgg gagatctccc gatcccctat ggtcgactct cagtacaatc tgctctgatg       60

ccgcatagtt aagccagtat ctgctccctg cttgtgtgtt ggaggtcgct gagtagtgcg      120

cgagcaaaat ttaagctaca caaggcaag gcttgaccga caattgcatg aagaatctgc        180

ttagggttag gcgttttgcg ctgcttcgcg atgtacgggc cagatatacg cgttgacatt      240

gattattgac tagttattaa tagtaatcaa ttacggggtc attagttcat agcccatata      300

tggagttccg cgttacataa cttacggtaa atggcccgcc tggctgaccg cccaacgacc      360

cccgcccatt gacgtcaata atgacgtatg ttcccatagt aacgccaata gggactttcc      420

attgacgtca atgggtggac tatttacggt aaactgccca cttggcagta catcaagtgt      480

atcatatgcc aagtacgccc cctattgacg tcaatgacgg taaatggccc gcctggcatt      540

atgcccagta catgacctta tgggactttc ctacttggca gtacatctac gtattagtca      600

tcgctattac catggtgatg cggttttggc agtacatcaa tgggcgtgga tagcggtttg      660

actcacgggg atttccaagt ctccacccca ttgacgtcaa tgggagtttg ttttggcacc      720

aaaatcaacg ggactttcca aaatgtcgta caactccgc cccattgacg caaatgggcg         780

gtaggcgtgt acggtgggag gtctatataa gcagagctct ctggctaact agagaaccca      840

ctgcttactg gcttatcgaa attaatacga ctcactatag ggagacccaa gcttggtacc      900

gccgccgcc atg ggc aag agg tcc gcc ggc tca atc atg tgg ctc gcg agc      951
           Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala Ser
            1               5                   10

ttg gca gtt gtc ata gct ggt aca agc gct gtg acc ttg gtg cgg aaa       999
Leu Ala Val Val Ile Ala Gly Thr Ser Ala Val Thr Leu Val Arg Lys
15                  20                  25                  30

aac aga tgg ttg ctc cta aat gtg aca tct gag gac ctc ggg aaa aca      1047
Asn Arg Trp Leu Leu Leu Asn Val Thr Ser Glu Asp Leu Gly Lys Thr
                35                  40                  45

ttc tct gtg ggc aca ggc aac tgc aca aca aac att ttg gaa gcc aag      1095
Phe Ser Val Gly Thr Gly Asn Cys Thr Thr Asn Ile Leu Glu Ala Lys
            50                  55                  60
```

47

```
tac tgg tgc cca gac tca atg gaa tac aac tgt ccc aat ctc agt cca          1143
Tyr Trp Cys Pro Asp Ser Met Glu Tyr Asn Cys Pro Asn Leu Ser Pro
        65                  70                  75

aga gag gag cca gat gac att gat tgc tgg tgc tat ggg gtg gaa aac          1191
Arg Glu Glu Pro Asp Asp Ile Asp Cys Trp Cys Tyr Gly Val Glu Asn
        80                  85                  90

gtt aga gtc gca tat ggt aag tgt gac tca gca ggc agg tct agg agg          1239
Val Arg Val Ala Tyr Gly Lys Cys Asp Ser Ala Gly Arg Ser Arg Arg
95                  100                 105                 110

tca aga agg gcc att gac ttg cct acg cat gaa aac cat ggt ttg aag          1287
Ser Arg Arg Ala Ile Asp Leu Pro Thr His Glu Asn His Gly Leu Lys
                115                 120                 125

acc cgg caa gaa aaa tgg atg act gga aga atg ggt gaa agg caa ctc          1335
Thr Arg Gln Glu Lys Trp Met Thr Gly Arg Met Gly Glu Arg Gln Leu
                130                 135                 140

caa aag att gag aga tgg ttc gtg agg aac ccc ttt ttt gca gtg acg          1383
Gln Lys Ile Glu Arg Trp Phe Val Arg Asn Pro Phe Phe Ala Val Thr
                145                 150                 155

gct ctg acc att gcc tac ctt gtg gga agc aac atg acg caa cga gtc          1431
Ala Leu Thr Ile Ala Tyr Leu Val Gly Ser Asn Met Thr Gln Arg Val
        160                 165                 170

gtg att gcc cta ctg gtc ttg gct gtt ggt ccg gcc tac tca gct cac          1479
Val Ile Ala Leu Leu Val Leu Ala Val Gly Pro Ala Tyr Ser Ala His
175                 180                 185                 190

tgc att gga att act gac agg gat ttc att gag ggg gtg cat gga gga          1527
Cys Ile Gly Ile Thr Asp Arg Asp Phe Ile Glu Gly Val His Gly Gly
                195                 200                 205

act tgg gtt tca gct acc ctg gag caa gac aag tgt gtc act gtt atg          1575
Thr Trp Val Ser Ala Thr Leu Glu Gln Asp Lys Cys Val Thr Val Met
                210                 215                 220

gcc cct gac aag cct tca ttg gac atc tca cta gag aca gta gcc att          1623
Ala Pro Asp Lys Pro Ser Leu Asp Ile Ser Leu Glu Thr Val Ala Ile
                225                 230                 235

gat aga cct gct gag gtg agg aaa gtg tgt tac aat gca gtt ctc act          1671
Asp Arg Pro Ala Glu Val Arg Lys Val Cys Tyr Asn Ala Val Leu Thr
        240                 245                 250

cat gtg aag att aat gac aag tgc ccc agc act gga gag gcc cac cta          1719
His Val Lys Ile Asn Asp Lys Cys Pro Ser Thr Gly Glu Ala His Leu
255                 260                 265                 270

gct gaa gag aac gaa ggg gac aat gcg tgc aag cgc act tat tct gat          1767
Ala Glu Glu Asn Glu Gly Asp Asn Ala Cys Lys Arg Thr Tyr Ser Asp
                275                 280                 285

aga ggc tgg ggc aat ggc tgt ggc cta ttt ggg aaa ggg agc att gtg          1815
Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser Ile Val
                290                 295                 300
```

48

```
gca tgc gcc aaa ttc act tgt gcc aaa tcc atg agt ttg ttt gag gtt        1863
Ala Cys Ala Lys Phe Thr Cys Ala Lys Ser Met Ser Leu Phe Glu Val
        305             310             315

gat cag acc aaa att cag tat gtc atc aga gca caa ttg cat gta ggg        1911
Asp Gln Thr Lys Ile Gln Tyr Val Ile Arg Ala Gln Leu His Val Gly
        320             325             330

gcc aag cag gaa aat tgg act acc gac att aag act ctc aag ttt gat        1959
Ala Lys Gln Glu Asn Trp Thr Thr Asp Ile Lys Thr Leu Lys Phe Asp
335             340             345             350

gcc ctg tca ggc tcc cag gaa gtc gag ttc att ggg tat gga aaa gct        2007
Ala Leu Ser Gly Ser Gln Glu Val Glu Phe Ile Gly Tyr Gly Lys Ala
                355             360             365

aca ctg gaa tgc cag gtg caa act gcg gtg gac ttt ggt aac agt tac        2055
Thr Leu Glu Cys Gln Val Gln Thr Ala Val Asp Phe Gly Asn Ser Tyr
        370             375             380

atc gct gag atg gaa aca gag agc tgg ata gtg gac aga cag tgg gcc        2103
Ile Ala Glu Met Glu Thr Glu Ser Trp Ile Val Asp Arg Gln Trp Ala
        385             390             395

cag gac ttg acc ctg cca tgg cag agt gga agt ggc ggg gtg tgg aga        2151
Gln Asp Leu Thr Leu Pro Trp Gln Ser Gly Ser Gly Gly Val Trp Arg
        400             405             410

gag atg cat cat ctt gtc gaa ttt gaa cct ccg cat gcc gcc act atc        2199
Glu Met His His Leu Val Glu Phe Glu Pro Pro His Ala Ala Thr Ile
415             420             425             430

aga gta ctg gcc ctg gga aac cag gaa ggc tcc ttg aaa aca gct ctt        2247
Arg Val Leu Ala Leu Gly Asn Gln Glu Gly Ser Leu Lys Thr Ala Leu
                435             440             445

act ggc gca atg agg gtt aca aag gac aca aat gac aac aac ctt tac        2295
Thr Gly Ala Met Arg Val Thr Lys Asp Thr Asn Asp Asn Asn Leu Tyr
                450             455             460

aaa cta cat ggt gga cat gtt tct tgc aga gtg aaa ttg tca gct ttg        2343
Lys Leu His Gly Gly His Val Ser Cys Arg Val Lys Leu Ser Ala Leu
        465             470             475

aca ctc aag ggg aca tcc tac aaa ata tgc act gac aaa atg ttt ttt        2391
Thr Leu Lys Gly Thr Ser Tyr Lys Ile Cys Thr Asp Lys Met Phe Phe
        480             485             490

gtc aag aac cca act gac act ggc cat ggc act gtt gtg atg cag gtg        2439
Val Lys Asn Pro Thr Asp Thr Gly His Gly Thr Val Val Met Gln Val
495             500             505             510

aaa gtg tca aaa gga gcc ccc tgc agg att cca gtg ata gta gct gat        2487
Lys Val Ser Lys Gly Ala Pro Cys Arg Ile Pro Val Ile Val Ala Asp
                515             520             525

gat ctt aca gcg gca atc aat aaa ggc att ttg gtt aca gtt aac ccc        2535
Asp Leu Thr Ala Ala Ile Asn Lys Gly Ile Leu Val Thr Val Asn Pro
                530             535             540
```

49

```
atc gcc tca acc aat gat gat gaa gtg ctg att gag gtg aac cca cct      2583
Ile Ala Ser Thr Asn Asp Asp Glu Val Leu Ile Glu Val Asn Pro Pro
        545                 550                 555

ttt gga gac agc tac att atc gtt ggg aga gga gat tca cgt ctc act      2631
Phe Gly Asp Ser Tyr Ile Ile Val Gly Arg Gly Asp Ser Arg Leu Thr
        560                 565                 570

tac cag tgg cac aaa gag gga agc tca ata gga aag ttg ttc act cag      2679
Tyr Gln Trp His Lys Glu Gly Ser Ser Ile Gly Lys Leu Phe Thr Gln
575             580                 585                 590

acc atg aaa ggc gtg gaa cgc ctg gcc gtc atg gga gac acc gcc tgg      2727
Thr Met Lys Gly Val Glu Arg Leu Ala Val Met Gly Asp Thr Ala Trp
                595                 600                 605

gat ttc agc tcc gct gga ggg ttc ttc act tcg gtt ggg aaa gga att      2775
Asp Phe Ser Ser Ala Gly Gly Phe Phe Thr Ser Val Gly Lys Gly Ile
            610                 615                 620

cat acg gtg ttt ggc tct gcc ttt cag ggg cta ttt ggc ggc ttg aac      2823
His Thr Val Phe Gly Ser Ala Phe Gln Gly Leu Phe Gly Gly Leu Asn
        625                 630                 635

tgg ata aca aag gtc atc atg ggg gcg gta ctt ata tgg gtt ggc atc      2871
Trp Ile Thr Lys Val Ile Met Gly Ala Val Leu Ile Trp Val Gly Ile
    640                 645                 650

aac aca aga aac atg aca atg tcc atg agc atg atc ttg gta gga gtg      2919
Asn Thr Arg Asn Met Thr Met Ser Met Ser Met Ile Leu Val Gly Val
655                 660                 665                 670

atc atg atg ttt ttg tct cta gga gtt ggg gcg tgagcggccg ctcgagcatg    2972
Ile Met Met Phe Leu Ser Leu Gly Val Gly Ala
            675                 680

catctagagg gccctattct atagtgtcac ctaaatgcta gagctcgctg atcagcctcg    3032

actgtgcctt ctagttgcca gccatctgtt gtttgcccct ccccgtgcc ttccttgacc     3092

ctggaaggtg ccactcccac tgtcctttcc taataaaatg aggaaattgc atcgcattgt    3152

ctgagtaggt gtcattctat tctggggggt ggggtggggc aggacagcaa gggggaggat    3212

tgggaagaca atagcaggca tgctggggat gcggtgggct ctatggcttc tgaggcggaa    3272

agaacagctg cattaatgaa tcggccaacg cgcggggaga ggcggtttgc gtattgggcg    3332

ctcttccgct tcctcgctca ctgactcgct gcgctcggtc gttcggctgc ggcgagcggt    3392

atcagctcac tcaaaggcgg taatacggtt atccacagaa tcaggggata acgcaggaaa    3452

gaacatgtga gcaaaaggcc agcaaaaggc caggaaccgt aaaaaggccg cgttgctggc    3512

gtttttccat aggctccgcc cccctgacga gcatcacaaa aatcgacgct caagtcagag    3572

gtggcgaaac ccgacaggac tataaagata ccaggcgttt ccccctggaa gctccctcgt    3632

gcgctctcct gttccgaccc tgccgcttac cggatacctg tccgcctttc tcccttcggg    3692
```

50

```
aagcgtggcg ctttctcaat gctcacgctg taggtatctc agttcggtgt aggtcgttcg    3752

ctccaagctg ggctgtgtgc acgaaccccc cgttcagccc gaccgctgcg ccttatccgg    3812

taactatcgt cttgagtcca acccggtaag acacgactta tcgccactgg cagcagccac    3872

tggtaacagg attagcagag cgaggtatgt aggcggtgct acagagttct tgaagtggtg    3932

gcctaactac ggctacacta gaaggacagt atttggtatc tgcgctctgc tgaagccagt    3992

taccttcgga aaaagagttg gtagctcttg atccggcaaa caaaccaccg ctggtagcgg    4052

tggttttttt gtttgcaagc agcagattac gcgcagaaaa aaaggatctc aagaagatcc    4112

tttgatcttt tctacggggt ctgacgctca gtggaacgaa aactcacgtt aagggatttt    4172

ggtcatgaga ttatcaaaaa ggatcttcac ctagatcctt ttaaattaaa aatgaagttt    4232

taaatcaatc taaagtatat atgagtaaac ttggtctgac agttaccaat gcttaatcag    4292

tgaggcacct atctcagcga tctgtctatt tcgttcatcc atagttgcct gactccccgt    4352

cgtgtagata actacgatac gggagggctt accatctggc cccagtgctg caatgatacc    4412

gcgagaccca cgctcaccgg ctccagattt atcagcaata aaccagccag ccggaagggc    4472

cgagcgcaga agtggtcctg caactttatc cgcctccatc cagtctatta attgttgccg    4532

ggaagctaga gtaagtagtt cgccagttaa tagtttgcgc aacgttgttg ccattgctac    4592

aggcatcgtg gtgtcacgct cgtcgtttgg tatggcttca ttcagctccg gttcccaacg    4652

atcaaggcga gttacatgat cccccatgtt gtgcaaaaaa gcggttagct ccttcggtcc    4712

tccgatcgtt gtcagaagta agttggccgc agtgttatca ctcatggtta tggcagcact    4772

gcataattct cttactgtca tgccatccgt aagatgcttt tctgtgactg gtgagtactc    4832

aaccaagtca ttctgagaat agtgtatgcg gcgaccgagt tgctcttgcc cggcgtcaat    4892

acgggataat accgcgccac atagcagaac tttaaaagtg ctcatcattg gaaaacgttc    4952

ttcggggcga aaactctcaa ggatcttacc gctgttgaga tccagttcga tgtaacccac    5012

tcgtgcaccc aactgatctt cagcatcttt tactttcacc agcgtttctg ggtgagcaaa    5072

aacaggaagg caaaatgccg caaaaaaggg aataagggcg acacggaaat gttgaatact    5132

catactcttc cttttttcaat attattgaag catttatcag ggttattgtc tcatgagcgg    5192

atacatattt gaatgtattt agaaaaataa acaaataggg gttccgcgca catttccccg    5252

aaaagtgcca cctgacgtc                                                 5271
```

<210> 24
<211> 681
<212> PRT
<213> Artificial Sequence

51

<220>
<223> Description of artificial sequence; note = synthetic construct

<400> 24

Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala Ser Leu Ala
1   5   10   15

Val Val Ile Ala Gly Thr Ser Ala Val Thr Leu Val Arg Lys Asn Arg
            20   25   30

Trp Leu Leu Leu Asn Val Thr Ser Glu Asp Leu Gly Lys Thr Phe Ser
        35   40   45

Val Gly Thr Gly Asn Cys Thr Thr Asn Ile Leu Glu Ala Lys Tyr Trp
        50   55   60

Cys Pro Asp Ser Met Glu Tyr Asn Cys Pro Asn Leu Ser Pro Arg Glu
65   70   75   80

Glu Pro Asp Asp Ile Asp Cys Trp Cys Tyr Gly Val Glu Asn Val Arg
                85   90   95

Val Ala Tyr Gly Lys Cys Asp Ser Ala Gly Arg Ser Arg Arg Ser Arg
            100   105   110

Arg Ala Ile Asp Leu Pro Thr His Glu Asn His Gly Leu Lys Thr Arg
            115   120   125

Gln Glu Lys Trp Met Thr Gly Arg Met Gly Glu Arg Gln Leu Gln Lys
        130   135   140

Ile Glu Arg Trp Phe Val Arg Asn Pro Phe Phe Ala Val Thr Ala Leu
145   150   155   160

Thr Ile Ala Tyr Leu Val Gly Ser Asn Met Thr Gln Arg Val Val Ile
                165   170   175

Ala Leu Leu Val Leu Ala Val Gly Pro Ala Tyr Ser Ala His Cys Ile
            180   185   190

Gly Ile Thr Asp Arg Asp Phe Ile Glu Gly Val His Gly Gly Thr Trp
            195   200   205

Val Ser Ala Thr Leu Glu Gln Asp Lys Cys Val Thr Val Met Ala Pro
    210   215   220

52

```
Asp Lys Pro Ser Leu Asp Ile Ser Leu Glu Thr Val Ala Ile Asp Arg
225             230             235                     240


Pro Ala Glu Val Arg Lys Val Cys Tyr Asn Ala Val Leu Thr His Val
                245             250                     255


Lys Ile Asn Asp Lys Cys Pro Ser Thr Gly Glu Ala His Leu Ala Glu
                260             265                     270


Glu Asn Glu Gly Asp Asn Ala Cys Lys Arg Thr Tyr Ser Asp Arg Gly
            275             280             285


Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser Ile Val Ala Cys
    290             295             300


Ala Lys Phe Thr Cys Ala Lys Ser Met Ser Leu Phe Glu Val Asp Gln
305             310             315                     320


Thr Lys Ile Gln Tyr Val Ile Arg Ala Gln Leu His Val Gly Ala Lys
                325             330             335


Gln Glu Asn Trp Thr Thr Asp Ile Lys Thr Leu Lys Phe Asp Ala Leu
            340             345             350


Ser Gly Ser Gln Glu Val Glu Phe Ile Gly Tyr Gly Lys Ala Thr Leu
            355             360             365


Glu Cys Gln Val Gln Thr Ala Val Asp Phe Gly Asn Ser Tyr Ile Ala
    370             375             380


Glu Met Glu Thr Glu Ser Trp Ile Val Asp Arg Gln Trp Ala Gln Asp
385             390             395                     400


Leu Thr Leu Pro Trp Gln Ser Gly Ser Gly Gly Val Trp Arg Glu Met
                405             410             415


His His Leu Val Glu Phe Glu Pro Pro His Ala Ala Thr Ile Arg Val
            420             425             430


Leu Ala Leu Gly Asn Gln Glu Gly Ser Leu Lys Thr Ala Leu Thr Gly
            435             440             445


Ala Met Arg Val Thr Lys Asp Thr Asn Asp Asn Asn Leu Tyr Lys Leu
    450             455             460
```

53

His Gly Gly His Val Ser Cys Arg Val Lys Leu Ser Ala Leu Thr Leu
465   470   475   480

Lys Gly Thr Ser Tyr Lys Ile Cys Thr Asp Lys Met Phe Phe Val Lys
                485   490   495

Asn Pro Thr Asp Thr Gly His Gly Thr Val Val Met Gln Val Lys Val
                500   505   510

Ser Lys Gly Ala Pro Cys Arg Ile Pro Val Ile Val Ala Asp Asp Leu
                515   520   525

Thr Ala Ala Ile Asn Lys Gly Ile Leu Val Thr Val Asn Pro Ile Ala
        530   535   540

Ser Thr Asn Asp Asp Glu Val Leu Ile Glu Val Asn Pro Pro Phe Gly
545   550   555   560

Asp Ser Tyr Ile Ile Val Gly Arg Gly Asp Ser Arg Leu Thr Tyr Gln
                565   570   575

Trp His Lys Glu Gly Ser Ser Ile Gly Lys Leu Phe Thr Gln Thr Met
                580   585   590

Lys Gly Val Glu Arg Leu Ala Val Met Gly Asp Thr Ala Trp Asp Phe
        595   600   605

Ser Ser Ala Gly Gly Phe Phe Thr Ser Val Gly Lys Gly Ile His Thr
        610   615   620

Val Phe Gly Ser Ala Phe Gln Gly Leu Phe Gly Gly Leu Asn Trp Ile
625   630   635   640

Thr Lys Val Ile Met Gly Ala Val Leu Ile Trp Val Gly Ile Asn Thr
                645   650   655

Arg Asn Met Thr Met Ser Met Ser Met Ile Leu Val Gly Val Ile Met
                660   665   670

Met Phe Leu Ser Leu Gly Val Gly Ala
        675   680

<210>   25
<211>   35

54

<212>   DNA
<213>   Artificial Sequence

<220>
<223>   Description of artificial sequence; note = synthetic construct

<220>
<221>   misc_feature
<222>   (1)..(35)
<223>   POW 454

<400>   25
aaaagaaaaa gcgctaccac catccaccgg gacag   35

<210>   26
<211>   41
<212>   DNA
<213>   Artificial Sequence

<220>
<223>   Description of artificial sequence; note = synthetic construct

<220>
<221>   misc_feature
<222>   (1)..(41)
<223>   CPOW 2417

<400>   26
actgttaccc tcaaccccgt actcgccggc gaaaaagaaa a   41

<210>   27
<211>   24
<212>   PRT
<213>   Artificial Sequence

<220>
<223>   Description of artificial sequence; note = synthetic construct

<220>
<221>   misc_feature
<223>   Modified JE Signal

<400>   27

Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala Ser Leu Ala
1   5   10   15

Val Val Ile Ala Gly Thr Ser Ala
            20

<210>   28
<211>   36
<212>   DNA

55

```
<213>  Artificial Sequence

<220>
<223>  Description of artificial sequence; note = synthetic construct


<220>
<221>  misc_feature
<222>  (1)..(36)
<223>  YF 482

<400>  28
aaaagaaaaa gcgctgtgac cttggtgcgg aaaaac                              36


<210>  29
<211>  41
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Description of artificial sequence; note = synthetic construct


<220>
<221>  misc_feature
<222>  (1)..(41)
<223>  CYF 2433

<400>  29
acagagatcc tcaaccccgc actcgccggc gaaaaagaaa a                        41


<210>  30
<211>  41
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Description of artificial sequence; note = synthetic construct


<220>
<221>  misc_feature
<222>  (1)..(41)
<223>  SLE 463

<400>  30
aaaagaaaaa gcgctttgca gttatcaacc tatcagggga a                        41


<210>  31
<211>  40
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Description of artificial sequence; note = synthetic construct
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<220>
<221> misc_feature
<222> (1)..(40)
<223> CSLE 2477

<400> 31
accgttggtc gcacgttcgg actcgccggc gaaaagaaa   40

<210> 32
<211> 39
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note = synthetic construct

<400> 32

Leu Asp Thr Ile Asn Arg Arg Pro Ser Lys Lys Arg Gly Gly Thr Arg
1   5   10   15

Ser Leu Leu Gly Leu Ala Ala Leu Ile Gly Leu Ala Ser Ser Leu Gln
            20   25   30

Leu Leu Ser Thr Tyr Gln Gly
        35

<210> 33
<211> 24
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note = synthetic construct

<400> 33

Met Trp Leu Ala Ser Leu Ala Val Val Ile Ala Cys Ala Gly Ala Met
1   5   10   15

Lys Leu Ser Asn Phe Gln Gly Lys
            20

<210> 34
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note = synthetic construct

<400> 34

Met Asn Glu Gly Ser Ile Met Trp Leu Ala Ser Leu Ala Val Val Ile

```
1                5                    10                      15


Ala Cys Ala Gly Ala Met Lys Leu Ser Asn Phe Gln Gly Lys
            20                  25                  30
```

<210> 35
<211> 39
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note = synthetic construct

<400> 35

```
Met Gly Arg Lys Gln Asn Lys Arg Gly Gly Asn Glu Gly Ser Ile Met
1                5                    10                      15


Trp Leu Ala Ser Leu Ala Val Val Ile Ala Cys Ala Gly Ala Met Lys
            20                  25                  30


Leu Ser Asn Phe Gln Gly Lys
        35
```

<210> 36
<211> 34
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note = synthetic construct

<400> 36

```
Met Ser Lys Lys Arg Gly Gly Ser Glu Thr Ser Val Leu Met Val Ile
1                5                    10                      15


Phe Met Leu Ile Gly Phe Ala Ala Ala Leu Lys Leu Ser Asn Phe Gln
            20                  25                  30


Gly Lys
```

<210> 37
<211> 33
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note = synthetic construct

<400> 37

Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala Ser Leu Ala
1   5   10   15

Val Val Ile Ala Cys Ala Gly Ala Val Thr Leu Ser Asn Phe Gln Gly
                20   25   30

Lys

<210> 38
<211> 46
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note = synthetic construct

<400> 38

Met Asn Val Leu Arg Gly Phe Arg Lys Glu Ile Gly Arg Met Leu Asn
1   5   10   15

Ile Leu Asn Arg Arg Arg Arg Thr Ala Gly Met Ile Ile Met Leu Ile
                20   25   30

Pro Thr Val Met Ala Phe His Leu Thr Thr Arg Asn Gly Glu
                35   40   45

<210> 39
<211> 40
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note = synthetic construct

<400> 39

Met Val Gly Leu Gln Lys Arg Gly Lys Arg Arg Ser Ala Thr Asp Trp
1   5   10   15

Met Ser Trp Leu Leu Val Ile Thr Leu Leu Gly Met Thr Leu Ala Ala
                20   25   30

Thr Val Arg Lys Glu Arg Gly Asp
                35   40

<210> 40
<211> 24
<212> PRT

59

<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note = synthetic construct

<400> 40

```
Met Gly Trp Leu Leu Val Val Val Leu Leu Gly Val Thr Leu Ala Ala
1               5                   10                  15


Thr Val Arg Lys Glu Arg Gly Asp
            20
```

<210> 41
<211> 24
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note = synthetic construct

<400> 41

```
Met Ser Trp Leu Leu Val Ile Thr Leu Leu Gly Met Thr Ile Ala Ala
1               5                   10                  15


Thr Val Arg Lys Glu Arg Gly Asp
            20
```

<210> 42
<211> 5292
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note = synthetic construct

<220>
<221> CDS
<222> (910)..(2964)

<400> 42
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gacggatcgg gagatctccc gatcccctat ggtgcactct cagtacaatc tgctctgatg       60

ccgcatagtt aagccagtat ctgctccctg cttgtgtgtt ggaggtcgct gagtagtgcg      120

cgagcaaaat ttaagctaca acaaggcaag gcttgaccga caattgcatg aagaatctgc      180

ttagggttag gcgttttgcg ctgcttcgcg atgtacgggc cagatatacg cgttgacatt      240

gattattgac tagttattaa tagtaatcaa ttacggggtc attagttcat agcccatata      300

tggagttccg cgttacataa cttacggtaa atggcccgcc tggctgaccg cccaacgacc      360

cccgcccatt gacgtcaata atgacgtatg ttcccatagt aacgccaata gggactttcc      420
```

```
attgacgtca atgggtggag tatttacggt aaactgccca cttggcagta catcaagtgt    480

atcatatgcc aagtacgccc cctattgacg tcaatgacgg taaatggccc gcctggcatt    540

atgcccagta catgacctta tgggactttc ctacttggca gtacatctac gtattagtca    600

tcgctattac catggtgatg cggttttggc agtacatcaa tgggcgtgga tagcggtttg    660

actcacgggg atttccaagt ctccacccca ttgacgtcaa tgggagtttg ttttggcacc    720

aaaatcaacg ggactttcca aaatgtcgta acaactccgc cccattgacg caaatgggcg    780

gtaggcgtgt acggtgggag gtctatataa gcagagctct ctggctaact agagaaccca    840

ctgcttactg gcttatcgaa attaatacga ctcactatag ggagacccaa gcttggtacc    900
```

```
gccgccgcc atg ggc aag agg tcc gcc ggc tca atc atg tgg ctc gcg agc    951
           Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala Ser
            1               5                   10
```

```
ttg gca gtt gtc ata gct tgt gca ggc gcc ttc cat tta acc aca cgt     999
Leu Ala Val Val Ile Ala Cys Ala Gly Ala Phe His Leu Thr Thr Arg
15                  20                  25                  30
```

```
aac gga gaa cca cac atg atc gtc agc aga caa gag aaa ggg aaa agt    1047
Asn Gly Glu Pro His Met Ile Val Ser Arg Gln Glu Lys Gly Lys Ser
                35                  40                  45
```

```
ctt ctg ttt aaa aca gag gat ggc gtg aac atg tgt acc ctc atg gcc    1095
Leu Leu Phe Lys Thr Glu Asp Gly Val Asn Met Cys Thr Leu Met Ala
                50                  55                  60
```

```
atg gac ctt ggt gaa ttg tgt gaa gac aca atc acg tac aag tgt ccc    1143
Met Asp Leu Gly Glu Leu Cys Glu Asp Thr Ile Thr Tyr Lys Cys Pro
            65                  70                  75
```

```
ctt ctc agg cag aat gag cca gaa gac ata gac tgt tgg tgc aac tct    1191
Leu Leu Arg Gln Asn Glu Pro Glu Asp Ile Asp Cys Trp Cys Asn Ser
        80                  85                  90
```

```
acg tcc acg tgg gta act tat ggg acg tgt acc acc atg gga gaa cat    1239
Thr Ser Thr Trp Val Thr Tyr Gly Thr Cys Thr Thr Met Gly Glu His
95                  100                 105                 110
```

```
aga aga gaa aaa aga tca gtg gca ctc gtt cca cat gtg gga atg gga    1287
Arg Arg Glu Lys Arg Ser Val Ala Leu Val Pro His Val Gly Met Gly
                115                 120                 125
```

```
ctg gag aca cga act gaa aca tgg atg tca tca gaa ggg gcc tgg aaa    1335
Leu Glu Thr Arg Thr Glu Thr Trp Met Ser Ser Glu Gly Ala Trp Lys
            130                 135                 140
```

```
cat gtc cag aga att gaa act tgg atc ttg aga cat cca ggc ttc acc    1383
His Val Gln Arg Ile Glu Thr Trp Ile Leu Arg His Pro Gly Phe Thr
        145                 150                 155
```

```
atg atg gca gca atc ctg gca tac acc ata gga acg aca cat ttc caa    1431
Met Met Ala Ala Ile Leu Ala Tyr Thr Ile Gly Thr Thr His Phe Gln
    160                 165                 170
```

61

```
aga gcc ctg att ttc atc tta ctg aca gct gtc act cct tca atg aca      1479
Arg Ala Leu Ile Phe Ile Leu Leu Thr Ala Val Thr Pro Ser Met Thr
175             180             185             190

atg cgt tgc ata gga atg tca aat aga gac ttt gtg gaa ggg gtt tca      1527
Met Arg Cys Ile Gly Met Ser Asn Arg Asp Phe Val Glu Gly Val Ser
                195             200             205

gga gga agc tgg gtt gac ata gtc tta gaa cat gga agc tgt gtg acg      1575
Gly Gly Ser Trp Val Asp Ile Val Leu Glu His Gly Ser Cys Val Thr
                210             215             220

acg atg gca aaa aac aaa cca aca ttg gat ttt gaa ctg ata aaa aca      1623
Thr Met Ala Lys Asn Lys Pro Thr Leu Asp Phe Glu Leu Ile Lys Thr
                225             230             235

gaa gcc aaa cag cct gcc acc cta agg aag tac tgt ata gag gca aag      1671
Glu Ala Lys Gln Pro Ala Thr Leu Arg Lys Tyr Cys Ile Glu Ala Lys
        240             245             250

cta acc aac aca aca aca gaa tct cgc tgc cca aca caa ggg gaa ccc      1719
Leu Thr Asn Thr Thr Thr Glu Ser Arg Cys Pro Thr Gln Gly Glu Pro
255             260             265             270

agc cta aat gaa gag cag gac aaa agg ttc gtc tgc aaa cac tcc atg      1767
Ser Leu Asn Glu Glu Gln Asp Lys Arg Phe Val Cys Lys His Ser Met
                275             280             285

gta gac aga gga tgg gga aat gga tgt gga cta ttt gga aag gga ggc      1815
Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Gly
                290             295             300

att gtg acc tgt gct atg ttc aga tgc aaa aag aac atg gaa gga aaa      1863
Ile Val Thr Cys Ala Met Phe Arg Cys Lys Lys Asn Met Glu Gly Lys
            305             310             315

gtt gtg caa cca gaa aac ttg gaa tac acc att gtg ata aca cct cac      1911
Val Val Gln Pro Glu Asn Leu Glu Tyr Thr Ile Val Ile Thr Pro His
        320             325             330

tca ggg gaa gag cat gca gtc gga aat gac aca gga aaa cat ggc aag      1959
Ser Gly Glu Glu His Ala Val Gly Asn Asp Thr Gly Lys His Gly Lys
335             340             345             350

gaa atc aaa ata aca cca cag agt tcc atc aca gaa gca gaa ttg aca      2007
Glu Ile Lys Ile Thr Pro Gln Ser Ser Ile Thr Glu Ala Glu Leu Thr
                355             360             365

ggt tat ggc act gtc aca atg gag tgc tct cca aga acg ggc ctc gac      2055
Gly Tyr Gly Thr Val Thr Met Glu Cys Ser Pro Arg Thr Gly Leu Asp
                370             375             380

ttc aat gag atg gtg ttg ttg cag atg gaa aat aaa gct tgg ctg gtg      2103
Phe Asn Glu Met Val Leu Leu Gln Met Glu Asn Lys Ala Trp Leu Val
                385             390             395

cac agg caa tgg ttc cta gac ctg ccg tta cca tgg ttg ccc gga gcg      2151
His Arg Gln Trp Phe Leu Asp Leu Pro Leu Pro Trp Leu Pro Gly Ala
        400             405  .          410
```

62

```
gac aca caa ggg tca aat tgg ata cag aaa gag aca ttg gtc act ttc      2199
Asp Thr Gln Gly Ser Asn Trp Ile Gln Lys Glu Thr Leu Val Thr Phe
415                 420                 425                 430

aaa aat ccc cat gcg aag aaa cag gat gtt gtt gtt tta gga tcc caa      2247
Lys Asn Pro His Ala Lys Lys Gln Asp Val Val Val Leu Gly Ser Gln
                    435                 440                 445

gaa ggg gcc atg cac aca gca ctt aca ggg gcc aca gaa atc caa atg      2295
Glu Gly Ala Met His Thr Ala Leu Thr Gly Ala Thr Glu Ile Gln Met
                450                 455                 460

tca tca gga aac tta ctc ttc aca gga cat ctc aag tgc agg ctg aga      2343
Ser Ser Gly Asn Leu Leu Phe Thr Gly His Leu Lys Cys Arg Leu Arg
                465                 470                 475

atg gac aag cta cag ctc aaa gga atg tca tac tct atg tgc aca gga      2391
Met Asp Lys Leu Gln Leu Lys Gly Met Ser Tyr Ser Met Cys Thr Gly
        480                 485                 490

aag ttt aaa gtt gtg aag gaa ata gca gaa aca caa cat gga aca ata      2439
Lys Phe Lys Val Val Lys Glu Ile Ala Glu Thr Gln His Gly Thr Ile
495                 500                 505                 510

gtt atc aga gtg caa tat gaa ggg gac ggc tct cca tgc aag atc cct      2487
Val Ile Arg Val Gln Tyr Glu Gly Asp Gly Ser Pro Cys Lys Ile Pro
                515                 520                 525

ttt gag ata atg gat ttg gaa aaa aga cat gtc tta ggt cgc ctg att      2535
Phe Glu Ile Met Asp Leu Glu Lys Arg His Val Leu Gly Arg Leu Ile
                530                 535                 540

aca gtc aac cca att gtg aca gaa aaa gat agc cca gtc aac ata gaa      2583
Thr Val Asn Pro Ile Val Thr Glu Lys Asp Ser Pro Val Asn Ile Glu
                545                 550                 555

gca gaa cct cca ttc gga gac agc tac atc atc ata gga gta gag ccg      2631
Ala Glu Pro Pro Phe Gly Asp Ser Tyr Ile Ile Ile Gly Val Glu Pro
        560                 565                 570

gga caa ctg aag ctc aac tgg ttt aag aaa gga agt tct atc ggc caa      2679
Gly Gln Leu Lys Leu Asn Trp Phe Lys Lys Gly Ser Ser Ile Gly Gln
575                 580                 585                 590

atg ttt gag aca aca atg agg ggg gcg aag aga atg gcc att tta ggt      2727
Met Phe Glu Thr Thr Met Arg Gly Ala Lys Arg Met Ala Ile Leu Gly
                595                 600                 605

gac aca gcc tgg gat ttt gga tcc ttg gga gga gtg ttt aca tct ata      2775
Asp Thr Ala Trp Asp Phe Gly Ser Leu Gly Gly Val Phe Thr Ser Ile
                610                 615                 620

gga aag gct ctc cac caa gtc ttt gga gca atc tat gga gct gcc ttc      2823
Gly Lys Ala Leu His Gln Val Phe Gly Ala Ile Tyr Gly Ala Ala Phe
                625                 630                 635

agt ggg gtt tca tgg act atg aaa atc ctc ata gga gtc att atc aca      2871
Ser Gly Val Ser Trp Thr Met Lys Ile Leu Ile Gly Val Ile Ile Thr
        640                 645                 650
```

```
tgg ata gga atg aat tca cgc agc acc tca ctg tct gtg aca cta gta      2919
Trp Ile Gly Met Asn Ser Arg Ser Thr Ser Leu Ser Val Thr Leu Val
655                 660             665             670

ttg gtg gga att gtg aca ctg tat ttg gga gtc atg gtg cag gcc          2964
Leu Val Gly Ile Val Thr Leu Tyr Leu Gly Val Met Val Gln Ala
                675             680             685


taattagttg agcggccgct cgagcatgca tctagagggc cctattctat agtgtcacct    3024

aaatgctaga gctcgctgat cagcctcgac tgtgccttct agttgccagc catctgttgt    3084

ttgcccctcc cccgtgcctt ccttgaccct ggaaggtgcc actcccactg tcctttccta    3144

ataaaatgag gaaattgcat cgcattgtct gagtaggtgt cattctattc tggggggtgg    3204

ggtggggcag gacagcaagg gggaggattg gaagacaat agcaggcatg ctggggatgc     3264

ggtgggctct atggcttctg aggcggaaag aaccagctgc attaatgaat cggccaacgc    3324

gcggggagag gcggtttgcg tattgggcgc tcttccgctt cctcgctcac tgactcgctg    3384

cgctcggtcg ttcggctgcg gcgagcggta tcagctcact caaaggcggt aatacggtta    3444

tccacagaat caggggataa cgcaggaaag aacatgtgag caaaaggcca gcaaaaggcc    3504

aggaaccgta aaaaggccgc gttgctggcg tttttccata ggctccgccc ccctgacgag    3564

catcacaaaa atcgacgctc aagtcagagg tggcgaaacc cgacaggact ataaagatac    3624

caggcgtttc cccctggaag ctccctcgtg cgctctcctg ttccgaccct gccgcttacc    3684

ggatacctgt ccgcctttct cccttcggga agcgtggcgc tttctcatag ctcacgctgt    3744

aggtatctca gttcggtgta ggtcgttcgc tccaagctgg gctgtgtgca cgaacccccc    3804

gttcagcccg accgctgcgc cttatccggt aactatcgtc ttgagtccaa cccggtaaga    3864

cacgacttat cgccactggc agcagccact ggtaacagga ttagcagagc gaggtatgta    3924

ggcggtgcta cagagttctt gaagtggtgg cctaactacg gctacactag aagaacagta    3984

tttggtatct gcgctctgct gaagccagtt accttcggaa aaagagttgg tagctcttga    4044

tccggcaaac aaaccaccgc tggtagcggt ggtttttttg tttgcaagca gcagattacg    4104

cgcagaaaaa aaggatctca agaagatcct ttgatctttt ctacggggtc tgacgctcag    4164

tggaacgaaa actcacgtta agggattttg gtcatgagat tatcaaaaag gatcttcacc    4224

tagatccttt taaattaaaa atgaagtttt aaatcaatct aaagtatata tgagtaaact    4284

tggtctgaca gttaccaatg cttaatcagt gaggcaccta tctcagcgat ctgtctattt    4344

cgttcatcca tagttgcctg actccccgtc gtgtagataa ctacgatacg gagggctta    4404

ccatctggcc ccagtgctgc aatgataccg cgagacccac gctcaccggc tccagattta    4464

tcagcaataa accagccagc cggaagggcc gagcgcagaa gtggtcctgc aactttatcc    4524
```
64

```
gcctccatcc agtctattaa ttgttgccgg gaagctagag taagtagttc gccagttaat    4584

agtttgcgca acgttgttgc cattgctaca ggcatcgtgg tgtcacgctc gtcgtttggt    4644

atggcttcat tcagctccgg ttcccaacga tcaaggcgag ttacatgatc ccccatgttg    4704

tgcaaaaaag cggttagctc cttcggtcct ccgatcgttg tcagaagtaa gttggccgca    4764

gtgttatcac tcatggttat ggcagcactg cataattctc ttactgtcat gccatccgta    4824

agatgctttt ctgtgactgg tgagtactca accaagtcat tctgagaata gtgtatgcgg    4884

cgaccgagtt gctcttgccc ggcgtcaata cgggataata ccgcgccaca tagcagaact    4944

ttaaaagtgc tcatcattgg aaaacgttct tcggggcgaa aactctcaag gatcttaccg    5004

ctgttgagat ccagttcgat gtaacccact cgtgcaccca actgatcttc agcatctttt    5064

actttcacca gcgtttctgg gtgagcaaaa acaggaaggc aaaatgccgc aaaaaaggga    5124

ataagggcga cacggaaatg ttgaatactc atactcttcc tttttcaata ttattgaagc    5184

atttatcagg gttattgtct catgagcgga tacatatttg aatgtattta gaaaaataaa    5244

caaatagggg ttccgcgcac atttccccga aaagtgccac ctgacgtc               5292
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<210> 43
<211> 685
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note = synthetic construct

<400> 43

```
Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala Ser Leu Ala
1               5                   10                  15


Val Val Ile Ala Cys Ala Gly Ala Phe His Leu Thr Thr Arg Asn Gly
            20                  25                  30


Glu Pro His Met Ile Val Ser Arg Gln Glu Lys Gly Lys Ser Leu Leu
        35                  40                  45


Phe Lys Thr Glu Asp Gly Val Asn Met Cys Thr Leu Met Ala Met Asp
    50                  55                  60


Leu Gly Glu Leu Cys Glu Asp Thr Ile Thr Tyr Lys Cys Pro Leu Leu
65                  70                  75                  80


Arg Gln Asn Glu Pro Glu Asp Ile Asp Cys Trp Cys Asn Ser Thr Ser
                85                  90                  95
```

65

```
Thr Trp Val Thr Tyr Gly Thr Cys Thr Thr Met Gly Glu His Arg Arg
         100              105              110

Glu Lys Arg Ser Val Ala Leu Val Pro His Val Gly Met Gly Leu Glu
         115              120              125

Thr Arg Thr Glu Thr Trp Met Ser Ser Glu Gly Ala Trp Lys His Val
     130              135              140

Gln Arg Ile Glu Thr Trp Ile Leu Arg His Pro Gly Phe Thr Met Met
145              150              155              160

Ala Ala Ile Leu Ala Tyr Thr Ile Gly Thr Thr His Phe Gln Arg Ala
             165              170              175

Leu Ile Phe Ile Leu Leu Thr Ala Val Thr Pro Ser Met Thr Met Arg
             180              185              190

Cys Ile Gly Met Ser Asn Arg Asp Phe Val Glu Gly Val Ser Gly Gly
         195              200              205

Ser Trp Val Asp Ile Val Leu Glu His Gly Ser Cys Val Thr Thr Met
     210              215              220

Ala Lys Asn Lys Pro Thr Leu Asp Phe Glu Leu Ile Lys Thr Glu Ala
225              230              235              240

Lys Gln Pro Ala Thr Leu Arg Lys Tyr Cys Ile Glu Ala Lys Leu Thr
             245              250              255

Asn Thr Thr Thr Glu Ser Arg Cys Pro Thr Gln Gly Glu Pro Ser Leu
             260              265              270

Asn Glu Glu Gln Asp Lys Arg Phe Val Cys Lys His Ser Met Val Asp
         275              280              285

Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Gly Ile Val
     290              295              300

Thr Cys Ala Met Phe Arg Cys Lys Lys Asn Met Glu Gly Lys Val Val
305              310              315              320

Gln Pro Glu Asn Leu Glu Tyr Thr Ile Val Ile Thr Pro His Ser Gly
             325              330              335
```

66

```
Glu Glu His Ala Val Gly Asn Asp Thr Gly Lys His Gly Lys Glu Ile
        340                 345                 350

Lys Ile Thr Pro Gln Ser Ser Ile Thr Glu Ala Glu Leu Thr Gly Tyr
        355                 360                 365

Gly Thr Val Thr Met Glu Cys Ser Pro Arg Thr Gly Leu Asp Phe Asn
    370                 375                 380

Glu Met Val Leu Leu Gln Met Glu Asn Lys Ala Trp Leu Val His Arg
385                 390                 395                 400

Gln Trp Phe Leu Asp Leu Pro Leu Pro Trp Leu Pro Gly Ala Asp Thr
            405                 410                 415

Gln Gly Ser Asn Trp Ile Gln Lys Glu Thr Leu Val Thr Phe Lys Asn
            420                 425                 430

Pro His Ala Lys Lys Gln Asp Val Val Val Leu Gly Ser Gln Glu Gly
        435                 440                 445

Ala Met His Thr Ala Leu Thr Gly Ala Thr Glu Ile Gln Met Ser Ser
    450                 455                 460

Gly Asn Leu Leu Phe Thr Gly His Leu Lys Cys Arg Leu Arg Met Asp
465                 470                 475                 480

Lys Leu Gln Leu Lys Gly Met Ser Tyr Ser Met Cys Thr Gly Lys Phe
            485                 490                 495

Lys Val Val Lys Glu Ile Ala Glu Thr Gln His Gly Thr Ile Val Ile
            500                 505                 510

Arg Val Gln Tyr Glu Gly Asp Gly Ser Pro Cys Lys Ile Pro Phe Glu
        515                 520                 525

Ile Met Asp Leu Glu Lys Arg His Val Leu Gly Arg Leu Ile Thr Val
    530                 535                 540

Asn Pro Ile Val Thr Glu Lys Asp Ser Pro Val Asn Ile Glu Ala Glu
545                 550                 555                 560

Pro Pro Phe Gly Asp Ser Tyr Ile Ile Ile Gly Val Glu Pro Gly Gln
            565                 570                 575
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Leu Lys Leu Asn Trp Phe Lys Lys Gly Ser Ser Ile Gly Gln Met Phe
        580   585   590

Glu Thr Thr Met Arg Gly Ala Lys Arg Met Ala Ile Leu Gly Asp Thr
        595   600   605

Ala Trp Asp Phe Gly Ser Leu Gly Gly Val Phe Thr Ser Ile Gly Lys
    610   615   620

Ala Leu His Gln Val Phe Gly Ala Ile Tyr Gly Ala Ala Phe Ser Gly
625   630   635   640

Val Ser Trp Thr Met Lys Ile Leu Ile Gly Val Ile Ile Thr Trp Ile
                645   650   655

Gly Met Asn Ser Arg Ser Thr Ser Leu Ser Val Thr Leu Val Leu Val
            660   665   670

Gly Ile Val Thr Leu Tyr Leu Gly Val Met Val Gln Ala
            675   680   685

<210>   44
<211>   5293
<212>   DNA
<213>   Artificial Sequence

<220>
<223>   Description of artificial sequence; note = synthetic construct

<220>
<221>   CDS
<222>   (910)..(2964)

<400>   44
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ccgcatagtt aagccagtat ctgctccctg cttgtgtgtt ggaggtcgct gagtagtgcg   120

cgagcaaaat ttaagctaca caaggcaag gcttgaccga caattgcatg aagaatctgc   180

ttagggttag gcgttttgcg ctgcttcgcg atgtacgggc cagatatacg cgttgacatt   240

gattattgac tagttattaa tagtaatcaa ttacggggtc attagttcat agcccatata   300

tggagttccg cgttacataa cttacggtaa atggcccgcc tggctgaccg cccaacgacc   360

cccgcccatt gacgtcaata atgacgtatg ttcccatagt aacgccaata gggactttcc   420

attgacgtca atgggtggag tatttacggt aaactgccca cttggcagta catcaagtgt   480

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atcatatgcc aagtacgccc cctattgacg tcaatgacgg taaatggccc gcctggcatt    540

atgcccagta catgacctta tgggactttc ctacttggca gtacatctac gtattagtca    600

tcgctattac catggtgatg cggttttggc agtacatcaa tgggcgtgga tagcggtttg    660

actcacgggg atttccaagt ctccacccca ttgacgtcaa tgggagtttg ttttggcacc    720

aaaatcaacg ggactttcca aaatgtcgta caactccgc cccattgacg caaatgggcg    780

gtaggcgtgt acggtgggag gtctatataa gcagagctct ctggctaact agagaaccca    840

ctgcttactg gcttatcgaa attaatacga ctcactatag ggagacccaa gcttggtacc    900

gccgccgcc atg ggc aag agg tcc gcc ggc tca atc atg tgg ctc gcg agc    951
          Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala Ser
           1               5                   10

ttg gca gtt gtc ata gct tgt gca ggc gcc ttc cat tta acc aca cgt    999
Leu Ala Val Val Ile Ala Cys Ala Gly Ala Phe His Leu Thr Thr Arg
15                  20                  25                  30

aac gga gaa cca cac atg atc gtc agc aga caa gag aaa ggg aaa agt    1047
Asn Gly Glu Pro His Met Ile Val Ser Arg Gln Glu Lys Gly Lys Ser
                35                  40                  45

ctt ctg ttt aaa aca gag gat ggc gtg aac atg tgt acc ctc atg gcc    1095
Leu Leu Phe Lys Thr Glu Asp Gly Val Asn Met Cys Thr Leu Met Ala
            50                  55                  60

atg gac ctt ggt gaa ttg tgt gaa gac aca atc acg tac aag tgt ccc    1143
Met Asp Leu Gly Glu Leu Cys Glu Asp Thr Ile Thr Tyr Lys Cys Pro
        65                  70                  75

ctt ctc agg cag aat gag cca gaa gac ata gac tgt tgg tgc aac tct    1191
Leu Leu Arg Gln Asn Glu Pro Glu Asp Ile Asp Cys Trp Cys Asn Ser
    80                  85                  90

acg tcc acg tgg gta act tat ggg acg tgt acc acc atg gga gaa cat    1239
Thr Ser Thr Trp Val Thr Tyr Gly Thr Cys Thr Thr Met Gly Glu His
95                  100                 105                 110

aga aga gaa aaa aga tca gtg gca ctc gtt cca cat gtg gga atg gga    1287
Arg Arg Glu Lys Arg Ser Val Ala Leu Val Pro His Val Gly Met Gly
                115                 120                 125

ctg gag aca cga act gaa aca tgg atg tca tca gaa ggg gcc tgg aaa    1335
Leu Glu Thr Arg Thr Glu Thr Trp Met Ser Ser Glu Gly Ala Trp Lys
            130                 135                 140

cat gtc cag aga att gaa act tgg atc ttg aga cat cca ggc ttc acc    1383
His Val Gln Arg Ile Glu Thr Trp Ile Leu Arg His Pro Gly Phe Thr
        145                 150                 155

atg atg gca gca atc ctg gca tac acc ata gga acg aca cat ttc caa    1431
Met Met Ala Ala Ile Leu Ala Tyr Thr Ile Gly Thr Thr His Phe Gln
    160                 165                 170

aga gcc ctg att ttc atc tta ctg aca gct gtc act cct tca atg aca    1479
Arg Ala Leu Ile Phe Ile Leu Leu Thr Ala Val Thr Pro Ser Met Thr
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69

atg cgt tgc ata gga atg tca aat aga gac ttt gtg gaa ggg gtt tca   1527
Met Arg Cys Ile Gly Met Ser Asn Arg Asp Phe Val Glu Gly Val Ser
            195   200   205

gga gga agc tgg gtt gac ata gtc tta gaa cat gga agc tgt gtg acg   1575
Gly Gly Ser Trp Val Asp Ile Val Leu Glu His Gly Ser Cys Val Thr
            210   215   220

acg atg gca aaa aac aaa cca aca ttg gat ttt gaa ctg ata aaa aca   1623
Thr Met Ala Lys Asn Lys Pro Thr Leu Asp Phe Glu Leu Ile Lys Thr
            225   230   235

gaa gcc aaa cag cct gcc acc cta agg aag tac tgt ata gag gca aag   1671
Glu Ala Lys Gln Pro Ala Thr Leu Arg Lys Tyr Cys Ile Glu Ala Lys
            240   245   250

cta acc aac aca aca aca gaa tct cgc tgc cca aca caa ggg gaa ccc   1719
Leu Thr Asn Thr Thr Thr Glu Ser Arg Cys Pro Thr Gln Gly Glu Pro
255   260   265   270

agc cta aat gaa gag cag gac aaa agg ttc gtc tgc aaa cac tcc atg   1767
Ser Leu Asn Glu Glu Gln Asp Lys Arg Phe Val Cys Lys His Ser Met
            275   280   285

gta gac aga gga tgg gga aat gga tgt gga cta ttt gga aag gga ggc   1815
Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Gly
            290   295   300

att gtg acc tgt gct atg ttc aga tgc aaa aag aac atg gaa gga aaa   1863
Ile Val Thr Cys Ala Met Phe Arg Cys Lys Lys Asn Met Glu Gly Lys
            305   310   315

gtt gtg caa cca gaa aac ttg gaa tac acc att gtg ata aca cct cac   1911
Val Val Gln Pro Glu Asn Leu Glu Tyr Thr Ile Val Ile Thr Pro His
            320   325   330

tca ggg gaa gag cat gca gtc gga aat gac aca gga aaa cat ggc aag   1959
Ser Gly Glu Glu His Ala Val Gly Asn Asp Thr Gly Lys His Gly Lys
335   340   345   350

gaa atc aaa ata aca cca cag agt tcc atc aca gaa gca gaa ttg aca   2007
Glu Ile Lys Ile Thr Pro Gln Ser Ser Ile Thr Glu Ala Glu Leu Thr
            355   360   365

ggt tat ggc act gtc aca atg gag tgc tct cca aga acg ggc ctc gac   2055
Gly Tyr Gly Thr Val Thr Met Glu Cys Ser Pro Arg Thr Gly Leu Asp
            370   375   380

ttc aat gag atg gtg ttg ttg cag atg gaa aat aaa gct tgg ctg gtg   2103
Phe Asn Glu Met Val Leu Leu Gln Met Glu Asn Lys Ala Trp Leu Val
            385   390   395

cac agg caa tgg ttc cta gac ctg ccg tta cca tgg ttg ccc gga gcg   2151
His Arg Gln Trp Phe Leu Asp Leu Pro Leu Pro Trp Leu Pro Gly Ala
            400   405   410

gac aca caa ggg tca aat tgg ata cag aaa gag aca ttg gtc act ttc   2199
Asp Thr Gln Gly Ser Asn Trp Ile Gln Lys Glu Thr Leu Val Thr Phe

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aaa aat ccc cat gcg aag aaa cag gat gtt gtt gtt tta gga tcc caa    2247
Lys Asn Pro His Ala Lys Lys Gln Asp Val Val Val Leu Gly Ser Gln
            435                 440                 445

gaa ggg gcc atg cac aca gca ctt aca ggg gcc aca gaa atc caa atg    2295
Glu Gly Ala Met His Thr Ala Leu Thr Gly Ala Thr Glu Ile Gln Met
            450                 455                 460

tca tca gga aac tta ctc ttc aca gga cat ctc aag tgc agg ctg aga    2343
Ser Ser Gly Asn Leu Leu Phe Thr Gly His Leu Lys Cys Arg Leu Arg
            465                 470                 475

atg gac aag cta cag ctc aaa gga atg tca tac tct atg tgc aca gga    2391
Met Asp Lys Leu Gln Leu Lys Gly Met Ser Tyr Ser Met Cys Thr Gly
            480                 485                 490

aag ttt aaa gtt gtg aag gaa ata gca gaa aca caa cat gga aca ata    2439
Lys Phe Lys Val Val Lys Glu Ile Ala Glu Thr Gln His Gly Thr Ile
495                 500                 505                 510

gtt atc aga gtg caa tat gaa ggg gac ggc tct cca tgc aag atc cct    2487
Val Ile Arg Val Gln Tyr Glu Gly Asp Gly Ser Pro Cys Lys Ile Pro
                515                 520                 525

ttt gag ata atg gat ttg gaa aaa aga cat gtc tta ggt cgc ctg att    2535
Phe Glu Ile Met Asp Leu Glu Lys Arg His Val Leu Gly Arg Leu Ile
            530                 535                 540

aca gtc aac cca att gtg aca gaa aaa gat agc cca gtc aac ata gaa    2583
Thr Val Asn Pro Ile Val Thr Glu Lys Asp Ser Pro Val Asn Ile Glu
            545                 550                 555

gca gaa cct cca ttc gga gac agc cac atc atc ata gga gta gag ccg    2631
Ala Glu Pro Pro Phe Gly Asp Ser His Ile Ile Ile Gly Val Glu Pro
            560                 565                 570

gga caa ctg aag ctc aac tgg ttt aag aaa gga agt tct atc ggc caa    2679
Gly Gln Leu Lys Leu Asn Trp Phe Lys Lys Gly Ser Ser Ile Gly Gln
575                 580                 585                 590

atg ttt gag aca aca atg agg ggg gcg aag aga atg gcc att tta ggt    2727
Met Phe Glu Thr Thr Met Arg Gly Ala Lys Arg Met Ala Ile Leu Gly
                595                 600                 605

gac aca gcc tgg gat ttt gga tcc ttg gga gga gtg ttt aca tct ata    2775
Asp Thr Ala Trp Asp Phe Gly Ser Leu Gly Gly Val Phe Thr Ser Ile
            610                 615                 620

gga aag gct ctc cac caa gtg ttt ggt ggt gcc ttc aga aca ctc ttt    2823
Gly Lys Ala Leu His Gln Val Phe Gly Gly Ala Phe Arg Thr Leu Phe
            625                 630                 635

ggg gga atg tct tgg atc aca caa ggg cta atg ggt gcc cta ctg ctc    2871
Gly Gly Met Ser Trp Ile Thr Gln Gly Leu Met Gly Ala Leu Leu Leu
            640                 645                 650

tgg atg ggc gtc aac gca cga gac cga tca att gct ttg gcc ttc tta    2919
Trp Met Gly Val Asn Ala Arg Asp Arg Ser Ile Ala Leu Ala Phe Leu
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gcc aca ggg ggt gtg ctc gtg ttc tta gcg acc aat gtg cat gct        2964
Ala Thr Gly Gly Val Leu Val Phe Leu Ala Thr Asn Val His Ala
                    675                    680                    685
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taattagttt gggcggccgc tcgagcatgc atctagaggg ccctattcta tagtgtcacc   3024

taaatgctag agctcgctga tcagcctcga ctgtgccttc tagttgccag ccatctgttg   3084

tttgcccctc ccccgtgcct tccttgaccc tggaaggtgc cactcccact gtcctttcct   3144

aataaaatga ggaaattgca tcgcattgtc tgagtaggtg tcattctatt ctggggggtg   3204

gggtggggca ggacagcaag ggggaggatt gggaagacaa tagcaggcat gctggggatg   3264

cggtgggctc tatggcttct gaggcggaaa gaaccagctg cattaatgaa tcggccaacg   3324

cgcggggaga ggcggtttgc gtattgggcg ctcttccgct tcctcgctca ctgactcgct   3384

gcgctcggtc gttcggctgc ggcgagcggt atcagctcac tcaaaggcgg taatacggtt   3444

atccacagaa tcaggggata acgcaggaaa gaacatgtga gcaaaaggcc agcaaaaggc   3504

caggaaccgt aaaaaggccg cgttgctggc gtttttccat aggctccgcc ccctgacga   3564

gcatcacaaa aatcgacgct caagtcagag gtggcgaaac ccgacaggac tataaagata   3624

ccaggcgttt cccctggaa gctccctcgt gcgctctcct gttccgaccc tgccgcttac   3684

cggatacctg tccgccttc tcccttcggg aagcgtggcg ctttctcata gctcacgctg   3744

taggtatctc agttcggtgt aggtcgttcg ctccaagctg ggctgtgtgc acgaacccc   3804

cgttcagccc gaccgctgcg ccttatccgg taactatcgt cttgagtcca acccggtaag   3864

acacgactta tcgccactgg cagcagccac tggtaacagg attagcagag cgaggtatgt   3924

aggcggtgct acagagttct tgaagtggtg gcctaactac ggctacacta gaagaacagt   3984

atttggtatc tgcgctctgc tgaagccagt taccttcgga aaaagagttg gtagctcttg   4044

atccggcaaa caaaccaccg ctggtagcgg tggttttttt gtttgcaagc agcagattac   4104

gcgcagaaaa aaaggatctc aagaagatcc tttgatcttt tctacggggt ctgacgctca   4164

gtggaacgaa aactcacgtt aagggatttt ggtcatgaga ttatcaaaaa ggatcttcac   4224

ctagatcctt ttaaattaaa aatgaagttt taaatcaatc taaagtatat atgagtaaac   4284

ttggtctgac agttaccaat gcttaatcag tgaggcacct atctcagcga tctgtctatt   4344

tcgttcatcc atagttgcct gactccccgt cgtgtagata actacgatac gggagggctt   4404

accatctggc cccagtgctg caatgatacc gcgagaccca cgctcaccgg ctccagattt   4464

atcagcaata aaccagccag ccggaagggc cgagcgcaga agtggtcctg caactttatc   4524

cgcctccatc cagtctatta attgttgccg ggaagctaga gtaagtagtt cgccagttaa   4584
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72

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tagtttgcgc aacgttgttg ccattgctac aggcatcgtg gtgtcacgct cgtcgtttgg   4644

tatggcttca ttcagctccg gttcccaacg atcaaggcga gttacatgat cccccatgtt   4704

gtgcaaaaaa gcggttagct ccttcggtcc tccgatcgtt gtcagaagta agttggccgc   4764

agtgttatca ctcatggtta tggcagcact gcataattct cttactgtca tgccatccgt   4824

aagatgcttt tctgtgactg gtgagtactc aaccaagtca ttctgagaat agtgtatgcg   4884

gcgaccgagt tgctcttgcc cggcgtcaat acgggataat accgcgccac atagcagaac   4944

tttaaaagtg ctcatcattg gaaaacgttc ttcggggcga aaactctcaa ggatcttacc   5004

gctgttgaga tccagttcga tgtaacccac tcgtgcaccc aactgatctt cagcatcttt   5064

tactttcacc agcgtttctg ggtgagcaaa aacaggaagg caaaatgccg caaaaaaggg   5124

aataagggcg acacggaaat gttgaatact catactcttc ctttttcaat attattgaag   5184

catttatcag ggttattgtc tcatgagcgg atacatattt gaatgtattt agaaaaataa   5244

acaaataggg gttccgcgca catttccccg aaaagtgcca cctgacgtc            5293
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<210> 45
<211> 685
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note = synthetic construct

<400> 45

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Val Val Ile Ala Cys Ala Gly Ala Phe His Leu Thr Thr Arg Asn Gly
            20                  25                  30


Glu Pro His Met Ile Val Ser Arg Gln Glu Lys Gly Lys Ser Leu Leu
        35                  40                  45


Phe Lys Thr Glu Asp Gly Val Asn Met Cys Thr Leu Met Ala Met Asp
    50                  55                  60


Leu Gly Glu Leu Cys Glu Asp Thr Ile Thr Tyr Lys Cys Pro Leu Leu
65                  70                  75                  80


Arg Gln Asn Glu Pro Glu Asp Ile Asp Cys Trp Cys Asn Ser Thr Ser
                85                  90                  95


Thr Trp Val Thr Tyr Gly Thr Cys Thr Thr Met Gly Glu His Arg Arg
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Glu Lys Arg Ser Val Ala Leu Val Pro His Val Gly Met Gly Leu Glu
    115   120   125

Thr Arg Thr Glu Thr Trp Met Ser Ser Glu Gly Ala Trp Lys His Val
    130   135   140

Gln Arg Ile Glu Thr Trp Ile Leu Arg His Pro Gly Phe Thr Met Met
145   150   155   160

Ala Ala Ile Leu Ala Tyr Thr Ile Gly Thr Thr His Phe Gln Arg Ala
    165   170   175

Leu Ile Phe Ile Leu Leu Thr Ala Val Thr Pro Ser Met Thr Met Arg
    180   185   190

Cys Ile Gly Met Ser Asn Arg Asp Phe Val Glu Gly Val Ser Gly Gly
    195   200   205

Ser Trp Val Asp Ile Val Leu Glu His Gly Ser Cys Val Thr Thr Met
    210   215   220

Ala Lys Asn Lys Pro Thr Leu Asp Phe Glu Leu Ile Lys Thr Glu Ala
225   230   235   240

Lys Gln Pro Ala Thr Leu Arg Lys Tyr Cys Ile Glu Ala Lys Leu Thr
    245   250   255

Asn Thr Thr Thr Glu Ser Arg Cys Pro Thr Gln Gly Glu Pro Ser Leu
    260   265   270

Asn Glu Glu Gln Asp Lys Arg Phe Val Cys Lys His Ser Met Val Asp
    275   280   285

Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Gly Ile Val
    290   295   300

Thr Cys Ala Met Phe Arg Cys Lys Lys Asn Met Glu Gly Lys Val Val
305   310   315   320

Gln Pro Glu Asn Leu Glu Tyr Thr Ile Val Ile Thr Pro His Ser Gly
    325   330   335

Glu Glu His Ala Val Gly Asn Asp Thr Gly Lys His Gly Lys Glu Ile

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Lys Ile Thr Pro Gln Ser Ser Ile Thr Glu Ala Glu Leu Thr Gly Tyr
        355   360   365

Gly Thr Val Thr Met Glu Cys Ser Pro Arg Thr Gly Leu Asp Phe Asn
        370   375   380

Glu Met Val Leu Leu Gln Met Glu Asn Lys Ala Trp Leu Val His Arg
385   390   395   400

Gln Trp Phe Leu Asp Leu Pro Leu Pro Trp Leu Pro Gly Ala Asp Thr
                405   410   415

Gln Gly Ser Asn Trp Ile Gln Lys Glu Thr Leu Val Thr Phe Lys Asn
                420   425   430

Pro His Ala Lys Lys Gln Asp Val Val Val Leu Gly Ser Gln Glu Gly
        435   440   445

Ala Met His Thr Ala Leu Thr Gly Ala Thr Glu Ile Gln Met Ser Ser
        450   455   460

Gly Asn Leu Leu Phe Thr Gly His Leu Lys Cys Arg Leu Arg Met Asp
465   470   475   480

Lys Leu Gln Leu Lys Gly Met Ser Tyr Ser Met Cys Thr Gly Lys Phe
                485   490   495

Lys Val Val Lys Glu Ile Ala Glu Thr Gln His Gly Thr Ile Val Ile
                500   505   510

Arg Val Gln Tyr Glu Gly Asp Gly Ser Pro Cys Lys Ile Pro Phe Glu
                515   520   525

Ile Met Asp Leu Glu Lys Arg His Val Leu Gly Arg Leu Ile Thr Val
        530   535   540

Asn Pro Ile Val Thr Glu Lys Asp Ser Pro Val Asn Ile Glu Ala Glu
545   550   555   560

Pro Pro Phe Gly Asp Ser His Ile Ile Ile Gly Val Glu Pro Gly Gln
                565   570   575

Leu Lys Leu Asn Trp Phe Lys Lys Gly Ser Ser Ile Gly Gln Met Phe

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Glu Thr Thr Met Arg Gly Ala Lys Arg Met Ala Ile Leu Gly Asp Thr
        595                 600                 605


Ala Trp Asp Phe Gly Ser Leu Gly Gly Val Phe Thr Ser Ile Gly Lys
    610                 615                 620


Ala Leu His Gln Val Phe Gly Gly Ala Phe Arg Thr Leu Phe Gly Gly
625                 630                 635                 640


Met Ser Trp Ile Thr Gln Gly Leu Met Gly Ala Leu Leu Leu Trp Met
                645                 650                 655


Gly Val Asn Ala Arg Asp Arg Ser Ile Ala Leu Ala Phe Leu Ala Thr
        660                 665                 670


Gly Gly Val Leu Val Phe Leu Ala Thr Asn Val His Ala
    675                 680                 685
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<210>  46
<211>  5293
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Description of artificial sequence; note = synthetic construct


<220>
<221>  CDS
<222>  (910)..(2964)

<400>  46
gacggatcgg gagatctccc gatcccctat ggtcgactct cagtacaatc tgctctgatg      60

ccgcatagtt aagccagtat ctgctccctg cttgtgtgtt ggaggtcgct gagtagtgcg     120

cgagcaaaat ttaagctaca acaaggcaag gcttgaccga caattgcatg aagaatctgc     180

ttagggttag gcgttttgcg ctgcttcgcg atgtacgggc cagatatacg cgttgacatt     240

gattattgac tagttattaa tagtaatcaa ttacggggtc attagttcat agcccatata     300

tggagttccg cgttacataa cttacggtaa atggcccgcc tggctgaccg cccaacgacc     360

cccgcccatt gacgtcaata atgacgtatg ttcccatagt aacgccaata gggactttcc     420

attgacgtca atgggtggac tatttacggt aaactgccca cttggcagta catcaagtgt     480

atcatatgcc aagtacgccc cctattgacg tcaatgacgg taaatggccc gcctggcatt     540

atgcccagta catgacctta tgggactttc ctacttggca gtacatctac gtattagtca     600
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                                  76

tcgctattac catggtgatg cggttttggc agtacatcaa tgggcgtgga tagcggtttg   660

actcacgggg atttccaagt ctccacccca ttgacgtcaa tgggagtttg ttttggcacc   720

aaaatcaacg ggactttcca aaatgtcgta acaactccgc cccattgacg caaatgggcg   780

gtaggcgtgt acggtgggag gtctatataa gcagagctct ctggctaact agagaaccca   840

ctgcttactg gcttatcgaa attaatacga ctcactatag ggagacccaa gcttggtacc'   900

gccgccgcc atg ggc aag agg tcc gcc ggc tca atc atg tgg ctc gcg agc   951
           Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala Ser
            1   5   10

ttg gca gtt gtc ata gct tgt gca ggc gcc ttc cat tta acc aca cgt   999
Leu Ala Val Val Ile Ala Cys Ala Gly Ala Phe His Leu Thr Thr Arg
15   20   25   30

aac gga gaa cca cac atg atc gtc agc aga caa gag aaa ggg aaa agt   1047
Asn Gly Glu Pro His Met Ile Val Ser Arg Gln Glu Lys Gly Lys Ser
                35   40   45

ctt ctg ttt aaa aca gag gat ggc gtg aac atg tgt acc ctc atg gcc   1095
Leu Leu Phe Lys Thr Glu Asp Gly Val Asn Met Cys Thr Leu Met Ala
             50   55   60

atg gac ctt ggt gaa ttg tgt gaa gac aca atc acg tac aag tgt ccc   1143
Met Asp Leu Gly Glu Leu Cys Glu Asp Thr Ile Thr Tyr Lys Cys Pro
         65   70   75

ctt ctc agg cag aat gag cca gaa gac ata gac tgt tgg tgc aac tct   1191
Leu Leu Arg Gln Asn Glu Pro Glu Asp Ile Asp Cys Trp Cys Asn Ser
     80   85   90

acg tcc acg tgg gta act tat ggg acg tgt acc acc atg gga gaa cat   1239
Thr Ser Thr Trp Val Thr Tyr Gly Thr Cys Thr Thr Met Gly Glu His
95   100   105   110

aga aga gaa aaa aga tca gtg gca ctc gtt cca cat gtg gga atg gga   1287
Arg Arg Glu Lys Arg Ser Val Ala Leu Val Pro His Val Gly Met Gly
                115   120   125

ctg gag aca cga act gaa aca tgg atg tca tca gaa ggg gcc tgg aaa   1335
Leu Glu Thr Arg Thr Glu Thr Trp Met Ser Ser Glu Gly Ala Trp Lys
             130   135   140

cat gtc cag aga att gaa act tgg atc ttg aga cat cca ggc ttc acc   1383
His Val Gln Arg Ile Glu Thr Trp Ile Leu Arg His Pro Gly Phe Thr
         145   150   155

atg atg gca gca atc ctg gca tac acc ata gga acg aca cat ttc caa   1431
Met Met Ala Ala Ile Leu Ala Tyr Thr Ile Gly Thr Thr His Phe Gln
     160   165   170

aga gcc ctg att ttc atc tta ctg aca gct gtc act cct tca atg aca   1479
Arg Ala Leu Ile Phe Ile Leu Leu Thr Ala Val Thr Pro Ser Met Thr
175   180   185   190

atg cgt tgc ata gga atg tca aat aga gac ttt gtg gaa ggg gtt tca   1527

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        Met Arg Cys Ile Gly Met Ser Asn Arg Asp Phe Val Glu Gly Val Ser
                        195                 200                 205

 gga gga agc tgg gtt gac ata gtc tta gaa cat ggg agc tgt gtg acg       1575
Gly Gly Ser Trp Val Asp Ile Val Leu Glu His Gly Ser Cys Val Thr
                210                 215                 220

acg atg gca aaa aac aaa cca aca ttg gat ttt gaa ctg ata aaa aca       1623
Thr Met Ala Lys Asn Lys Pro Thr Leu Asp Phe Glu Leu Ile Lys Thr
                225                 230                 235

gaa gcc aaa cag cct gcc acc cta agg aag tac tgt ata gag gca aag       1671
Glu Ala Lys Gln Pro Ala Thr Leu Arg Lys Tyr Cys Ile Glu Ala Lys
        240                 245                 250

cta acc aac aca aca aca gaa tct cgc tgc cca aca caa ggg gaa ccc       1719
Leu Thr Asn Thr Thr Thr Glu Ser Arg Cys Pro Thr Gln Gly Glu Pro
255                 260                 265                 270

agc cta aat gaa gag cag gac aaa agg ttc gtc tgc aaa cac tcc atg       1767
Ser Leu Asn Glu Glu Gln Asp Lys Arg Phe Val Cys Lys His Ser Met
                275                 280                 285

gta gac aga gga tgg gga aat gga tgt gga cta ttt gga aag gga ggc       1815
Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Gly
                290                 295                 300

att gtg acc tgt gct atg ttc aga tgc aaa aag aac atg gaa gga aaa       1863
Ile Val Thr Cys Ala Met Phe Arg Cys Lys Lys Asn Met Glu Gly Lys
                305                 310                 315

gtt gtg caa cca gaa aac ttg gaa tac acc att gtg ata aca cct cac       1911
Val Val Gln Pro Glu Asn Leu Glu Tyr Thr Ile Val Ile Thr Pro His
        320                 325                 330

tca ggg gaa gag cat gca gtc gga aat gac aca gga aaa cat ggc aag       1959
Ser Gly Glu Glu His Ala Val Gly Asn Asp Thr Gly Lys His Gly Lys
335                 340                 345                 350

gaa atc aaa ata aca cca cag agt tcc atc aca gaa gca gaa ttg aca       2007
Glu Ile Lys Ile Thr Pro Gln Ser Ser Ile Thr Glu Ala Glu Leu Thr
                355                 360                 365

ggt tat ggc act gtc aca atg gag tgc tct cca aga acg ggc ctc gac       2055
Gly Tyr Gly Thr Val Thr Met Glu Cys Ser Pro Arg Thr Gly Leu Asp
                370                 375                 380

ttc aat gag atg gtg ttg ttg cag atg gaa aat aaa gct tgg ctg gtg       2103
Phe Asn Glu Met Val Leu Leu Gln Met Glu Asn Lys Ala Trp Leu Val
                385                 390                 395

cac agg caa tgg ttc cta gac ctg ccg tta cca tgg ttg ccc gga gcg       2151
His Arg Gln Trp Phe Leu Asp Leu Pro Leu Pro Trp Leu Pro Gly Ala
        400                 405                 410

gac aca caa ggg tca aat tgg ata cag aaa gag aca ttg gtc act ttc       2199
Asp Thr Gln Gly Ser Asn Trp Ile Gln Lys Glu Thr Leu Val Thr Phe
415                 420                 425                 430

aaa aat ccc cat gcg aag aaa cag gat gtt gtt gtt tta gga tcc caa       2247
                                78
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Lys Asn Pro His Ala Lys Lys Gln Asp Val Val Val Leu Gly Ser Gln
            435                 440             445

gaa ggg gcc atg cac aca gca ctt aca ggg gcc aca gaa atc caa atg    2295
Glu Gly Ala Met His Thr Ala Leu Thr Gly Ala Thr Glu Ile Gln Met
            450                 455             460

tca tca gga aac tta ctc ttc aca gga cat ctc aag tgc agg ctg aga    2343
Ser Ser Gly Asn Leu Leu Phe Thr Gly His Leu Lys Cys Arg Leu Arg
            465                 470             475

atg gac aag cta cag ctc aaa gga atg tca tac tct atg tgc aca gga    2391
Met Asp Lys Leu Gln Leu Lys Gly Met Ser Tyr Ser Met Cys Thr Gly
        480                 485             490

aag ttt aaa gtt gtg aag gaa ata gca gaa aca caa cat gga aca ata    2439
Lys Phe Lys Val Val Lys Glu Ile Ala Glu Thr Gln His Gly Thr Ile
495                 500                 505             510

gtt atc aga gtg caa tat gaa ggg gac ggc tct cca tgc aag atc cct    2487
Val Ile Arg Val Gln Tyr Glu Gly Asp Gly Ser Pro Cys Lys Ile Pro
                515                 520             525

ttt gag ata atg gat ttg gaa aaa aga cat gtc tta ggt cgc ctg att    2535
Phe Glu Ile Met Asp Leu Glu Lys Arg His Val Leu Gly Arg Leu Ile
            530                 535             540

aca gtc aac cca att gtg aca gaa aaa gat agc cca gtc aac ata gaa    2583
Thr Val Asn Pro Ile Val Thr Glu Lys Asp Ser Pro Val Asn Ile Glu
            545                 550             555

gca gaa cct cca ttc gga gac agc tac atc atc ata gga gta gag ccg    2631
Ala Glu Pro Pro Phe Gly Asp Ser Tyr Ile Ile Ile Gly Val Glu Pro
        560                 565             570

gga caa ctg aag ctc aac tgg ttt aag aaa gga agc acg ctg ggc aag    2679
Gly Gln Leu Lys Leu Asn Trp Phe Lys Lys Gly Ser Thr Leu Gly Lys
575                 580                 585             590

gcc ttt tca aca act ttg aag gga gct caa aga ctg gca gcg ttg ggc    2727
Ala Phe Ser Thr Thr Leu Lys Gly Ala Gln Arg Leu Ala Ala Leu Gly
                595                 600             605

gac aca gcc tgg gac ttt ggc tct att gga ggg gtc ttc aac tcc ata    2775
Asp Thr Ala Trp Asp Phe Gly Ser Ile Gly Gly Val Phe Asn Ser Ile
            610                 615             620

gga aaa gcc gtt cac caa gtg ttt ggt ggt gcc ttc aga aca ctc ttt    2823
Gly Lys Ala Val His Gln Val Phe Gly Gly Ala Phe Arg Thr Leu Phe
            625                 630             635

ggg gga atg tct tgg atc aca caa ggg cta atg ggt gcc cta ctg ctc    2871
Gly Gly Met Ser Trp Ile Thr Gln Gly Leu Met Gly Ala Leu Leu Leu
            640                 645             650

tgg atg ggc gtc aac gca cga gac cga tca att gct ttg gcc ttc tta    2919
Trp Met Gly Val Asn Ala Arg Asp Arg Ser Ile Ala Leu Ala Phe Leu
655                 660                 665             670

gcc aca ggg ggt gtg ctc gtg ttc tta gcg acc aat gtg cat gct        2964
                            79
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Ala Thr Gly Gly Val Leu Val Phe Leu Ala Thr Asn Val His Ala
              675   680   685

taattagttt gagcggccgc tcgagcatgc atctagaggg ccctattcta tagtgtcacc   3024

taaatgctag agctcgctga tcagcctcga ctgtgccttc tagttgccag ccatctgttg   3084

tttgcccctc ccccgtgcct tccttgaccc tggaaggtgc cactcccact gtcctttcct   3144

aataaaatga ggaaattgca tcgcattgtc tgagtaggtg tcattctatt ctggggggtg   3204

gggtggggca ggacagcaag ggggaggatt gggaagacaa tagcaggcat gctggggatg   3264

cggtgggctc tatggcttct gaggcggaaa gaaccagctg cattaatgaa tcggccaacg   3324

cgcggggaga ggcggtttgc gtattgggcg ctcttccgct tcctcgctca ctgactcgct   3384

gcgctcggtc gttcggctgc ggcgagcggt atcagctcac tcaaaggcgg taatacggtt   3444

atccacagaa tcaggggata cgcaggaaa gaacatgtga gcaaaaggcc agcaaaaggc   3504

caggaaccgt aaaaaggccg cgttgctggc gttttccat aggctccgcc ccctgacga   3564

gcatcacaaa aatcgacgct caagtcagag gtggcgaaac ccgacaggac tataaagata   3624

ccaggcgttt cccctggaa gctccctcgt gcgctctcct gttccgaccc tgccgcttac   3684

cggatacctg tccgccttc tcccttcggg aagcgtggcg ctttctcaat gctcacgctg   3744

taggtatctc agttcggtgt aggtcgttcg ctccaagctg ggctgtgtgc acgaaccccc   3804

cgttcagccc gaccgctgcg ccttatccgg taactatcgt cttgagtcca acccggtaag   3864

acacgactta tcgccactgg cagcagccac tggtaacagg attagcagag cgaggtatgt   3924

aggcggtgct acagagttct tgaagtggtg gcctaactac ggctacacta gaaggacagt   3984

atttggtatc tgcgctctgc tgaagccagt taccttcgga aaaagagttg gtagctcttg   4044

atccggcaaa caaaccaccg ctggtagcgg tggttttttt gtttgcaagc agcagattac   4104

gcgcagaaaa aaaggatctc aagaagatcc tttgatcttt tctacggggt ctgacgctca   4164

gtggaacgaa aactcacgtt aagggatttt ggtcatgaga ttatcaaaaa ggatcttcac   4224

ctagatcctt ttaaattaaa aatgaagttt taaatcaatc taaagtatat atgagtaaac   4284

ttggtctgac agttaccaat gcttaatcag tgaggcacct atctcagcga tctgtctatt   4344

tcgttcatcc atagttgcct gactccccgt cgtgtagata actacgatac gggagggctt   4404

accatctggc cccagtgctg caatgatacc gcgagaccca cgctcaccgg ctccagattt   4464

atcagcaata aaccagccag ccggaagggc cgagcgcaga agtggtcctg caactttatc   4524

cgcctccatc cagtctatta attgttgccg ggaagctaga gtaagtagtt cgccagttaa   4584

tagtttgcgc aacgttgttg ccattgctac aggcatcgtg gtgtcacgct cgtcgtttgg   4644

tatggcttca ttcagctccg gttcccaacg atcaaggcga gttacatgat cccccatgtt   4704

80

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gtgcaaaaaa gcggttagct ccttcggtcc tccgatcgtt gtcagaagta agttggccgc    4764

agtgttatca ctcatggtta tggcagcact gcataattct cttactgtca tgccatccgt    4824

aagatgcttt tctgtgactg gtgagtactc aaccaagtca ttctgagaat agtgtatgcg    4884

gcgaccgagt tgctcttgcc cggcgtcaat acgggataat accgcgccac atagcagaac    4944

tttaaaagtg ctcatcattg gaaaacgttc ttcggggcga aaactctcaa ggatcttacc    5004

gctgttgaga tccagttcga tgtaacccac tcgtgcaccc aactgatctt cagcatcttt    5064

tactttcacc agcgtttctg ggtgagcaaa aacaggaagg caaaatgccg caaaaaaggg    5124

aataagggcg acacggaaat gttgaatact catactcttc cttttcaat attattgaag    5184

catttatcag ggttattgtc tcatgagcgg atacatattt gaatgtattt agaaaaataa    5244

acaaataggg gttccgcgca catttccccg aaaagtgcca cctgacgtc                5293
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<210> 47
<211> 685
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note = synthetic construct

<400> 47

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Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala Ser Leu Ala
1               5                   10                  15


Val Val Ile Ala Cys Ala Gly Ala Phe His Leu Thr Thr Arg Asn Gly
            20                  25                  30


Glu Pro His Met Ile Val Ser Arg Gln Glu Lys Gly Lys Ser Leu Leu
        35                  40                  45


Phe Lys Thr Glu Asp Gly Val Asn Met Cys Thr Leu Met Ala Met Asp
    50                  55                  60


Leu Gly Glu Leu Cys Glu Asp Thr Ile Thr Tyr Lys Cys Pro Leu Leu
65                  70                  75                  80


Arg Gln Asn Glu Pro Glu Asp Ile Asp Cys Trp Cys Asn Ser Thr Ser
                85                  90                  95


Thr Trp Val Thr Tyr Gly Thr Cys Thr Thr Met Gly Glu His Arg Arg
            100                 105                 110
```

81

Glu Lys Arg Ser Val Ala Leu Val Pro His Val Gly Met Gly Leu Glu
        115   120   125

Thr Arg Thr Glu Thr Trp Met Ser Ser Glu Gly Ala Trp Lys His Val
        130   135   140

Gln Arg Ile Glu Thr Trp Ile Leu Arg His Pro Gly Phe Thr Met Met
145   150   155   160

Ala Ala Ile Leu Ala Tyr Thr Ile Gly Thr Thr His Phe Gln Arg Ala
                165   170   175

Leu Ile Phe Ile Leu Leu Thr Ala Val Thr Pro Ser Met Thr Met Arg
                180   185   190

Cys Ile Gly Met Ser Asn Arg Asp Phe Val Glu Gly Val Ser Gly Gly
            195   200   205

Ser Trp Val Asp Ile Val Leu Glu His Gly Ser Cys Val Thr Thr Met
        210   215   220

Ala Lys Asn Lys Pro Thr Leu Asp Phe Glu Leu Ile Lys Thr Glu Ala
225   230   235   240

Lys Gln Pro Ala Thr Leu Arg Lys Tyr Cys Ile Glu Ala Lys Leu Thr
                245   250   255

Asn Thr Thr Thr Glu Ser Arg Cys Pro Thr Gln Gly Glu Pro Ser Leu
                260   265   270

Asn Glu Glu Gln Asp Lys Arg Phe Val Cys Lys His Ser Met Val Asp
            275   280   285

Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Gly Ile Val
        290   295   300

Thr Cys Ala Met Phe Arg Cys Lys Lys Asn Met Glu Gly Lys Val Val
305   310   315   320

Gln Pro Glu Asn Leu Glu Tyr Thr Ile Val Ile Thr Pro His Ser Gly
                325   330   335

Glu Glu His Ala Val Gly Asn Asp Thr Gly Lys His Gly Lys Glu Ile
            340   345   350

82

```
Lys Ile Thr Pro Gln Ser Ser Ile Thr Glu Ala Glu Leu Thr Gly Tyr
        355             360             365


Gly Thr Val Thr Met Glu Cys Ser Pro Arg Thr Gly Leu Asp Phe Asn
    370             375             380


Glu Met Val Leu Leu Gln Met Glu Asn Lys Ala Trp Leu Val His Arg
385             390             395             400


Gln Trp Phe Leu Asp Leu Pro Leu Pro Trp Leu Pro Gly Ala Asp Thr
            405             410             415


Gln Gly Ser Asn Trp Ile Gln Lys Glu Thr Leu Val Thr Phe Lys Asn
        420             425             430


Pro His Ala Lys Lys Gln Asp Val Val Val Leu Gly Ser Gln Glu Gly
        435             440             445


Ala Met His Thr Ala Leu Thr Gly Ala Thr Glu Ile Gln Met Ser Ser
    450             455             460


Gly Asn Leu Leu Phe Thr Gly His Leu Lys Cys Arg Leu Arg Met Asp
465             470             475             480


Lys Leu Gln Leu Lys Gly Met Ser Tyr Ser Met Cys Thr Gly Lys Phe
            485             490             495


Lys Val Val Lys Glu Ile Ala Glu Thr Gln His Gly Thr Ile Val Ile
            500             505             510


Arg Val Gln Tyr Glu Gly Asp Gly Ser Pro Cys Lys Ile Pro Phe Glu
            515             520             525


Ile Met Asp Leu Glu Lys Arg His Val Leu Gly Arg Leu Ile Thr Val
    530             535             540


Asn Pro Ile Val Thr Glu Lys Asp Ser Pro Val Asn Ile Glu Ala Glu
545             550             555             560


Pro Pro Phe Gly Asp Ser Tyr Ile Ile Ile Gly Val Glu Pro Gly Gln
            565             570             575


Leu Lys Leu Asn Trp Phe Lys Lys Gly Ser Thr Leu Gly Lys Ala Phe
        580             585             590


                                    83
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Ser Thr Thr Leu Lys Gly Ala Gln Arg Leu Ala Ala Leu Gly Asp Thr
        595   600   605

Ala Trp Asp Phe Gly Ser Ile Gly Gly Val Phe Asn Ser Ile Gly Lys
    610   615   620

Ala Val His Gln Val Phe Gly Gly Ala Phe Arg Thr Leu Phe Gly Gly
625   630   635   640

Met Ser Trp Ile Thr Gln Gly Leu Met Gly Ala Leu Leu Leu Trp Met
                645   650   655

Gly Val Asn Ala Arg Asp Arg Ser Ile Ala Leu Ala Phe Leu Ala Thr
        660   665   670

Gly Gly Val Leu Val Phe Leu Ala Thr Asn Val His Ala
        675   680   685

<210> 48
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note = synthetic construct

<400> 48
tgtgcaggcg ccttccattt aaccacacgt aacg   34

<210> 49
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note = synthetic construct

<400> 49
tcgagcggcc gctcaactaa ttaggcctgc accatgactc   40

<210> 50
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note = synthetic construct

<400> 50
cttatcgaaa ttaatacgac tcactatagg   30

<210> 51
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note = synthetic construct

<400> 51
atagattgct ccaaacactt ggtgg   25

<210> 52
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note = synthetic construct

<400> 52
actccatagg aaaagccgtt cacc   24

<210> 53
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note = synthetic construct

<400> 53
gcgagctcta gcatttaggt gacactatag   30

<210> 54
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note = synthetic construct

<400> 54
ctccaccaag tgtttggtgg tgccttcaga aca   33

<210> 55
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note = synthetic construct

<400> 55

Leu His Gln Val Phe Gly Gly Ala Phe Arg Thr
1   5   10

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<210>  56
<211>  30
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Description of artificial sequence; note = synthetic construct

<400>  56
cttatcgaaa ttaatacgac tcactatagg                                    30


<210>  57
<211>  39
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Description of artificial sequence; note = synthetic construct

<400>  57
gaattcgtct cacttccttt cttaaaccag ttgagcttc                          39


<210>  58
<211>  31
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Description of artificial sequence; note = synthetic construct

<400>  58
ggaattcgtc tcggaagcac gctgggcaag g                                  31


<210>  59
<211>  30
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Description of artificial sequence; note = synthetic construct

<400>  59
gcgagctcta gcatttaggt gacactatag                                    30


<210>  60
<211>  33
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Description of artificial sequence; note = synthetic construct

<400>  60
aactggttta agaaaggaag cacgctgggc gcc                                33
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<210>  61
<211>  11
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Description of artificial sequence; note = synthetic construct

<400>  61

Asn Trp Lys Lys Gly Ser Thr Leu Gly Lys Ala
1               5                   10
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